

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Description

(without alignment)
9356.731 million cell updates/sec

1 atgaagctctcgattct.....ttgagggttgaccctgtaa 444

Gapor 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters:

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing:	Minimum Match	0%
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Listing first 45 summaries

GenEmb1:*

- 1: gb_da.*
- 2: gb_hhg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_srs.*
- 11: gb_ssg.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vl.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_srs.*
- 28: em_un.*
- 29: em_vl.*
- 30: em_hhg_hum.*
- 31: em_hhg_inhv.*
- 32: em_hhg_other.*
- 33: em_hhg_mus.*
- 34: em_hhg_pln.*
- 35: em_hhg_rtd.*
- 36: em_hhg_mam.*
- 37: em_hhg_vrt.*
- 38: em_sy.*
- 39: em_hhg_hum.*
- 40: em_hhg_mus.*
- 41: em_hhg_other.*

SID-1 =
Known
analog
Cod. 502
Per 10307

Pred. No. is the number of results predicted by chance to have a

Result No.	Score	Query	Match	Length	DB	ID	Description
1	444	100.0	459	6	108377	I08377	Sequence 2
2	444	100.0	951	4	BOVLSZ2B	M26243	Bovine lyso
3	444	100.0	1060	6	BOVLSZ1A	L23758	Bos taurus
4	439	98.9	964	6	I12256	I12256	Sequence 1
5	437.4	98.5	909	4	BOVLSZ2A	M26241	Bovine lyso
6	437.4	98.5	963	6	I09315	I09315	Sequence 1
7	426.4	96.0	1082	4	BOVLSZ3A	M26242	Bovine lyso
8	420	94.6	891	4	BOVLSZ1B	M26246	Bovine lyso
9	416.8	93.9	906	4	BOVLSZ1A	M26245	Bovine lyso
10	397.4	89.5	877	4	BOVLSZ2C	M26244	Bovine lyso
11	367.6	82.8	875	4	SHPLZM3A	M2496	Sheep lysoz
12	367.6	82.8	881	4	SHPLZM1B	M32499	Sheep lysoz
13	367.6	82.8	881	4	SHPLZM1C	M32494	Sheep lysoz
14	367.6	82.8	881	4	SHPLZM2A	M32495	Sheep lysoz
15	366	82.4	881	4	SHPLZM1A	M32492	Sheep lysoz
16	364.4	82.1	875	4	SHPLZM4A	M32497	Sheep lysoz
17	364.4	82.1	875	4	SHPLZM4B	M32498	Sheep lysoz
18	353.2	79.5	885	4	AXILZM1	M32499	A. axis, lyso
19	351.6	79.2	873	4	AXILZM2	M32500	A. axis lyso
20	340	76.6	1248	4	BOVLSZM1AD	L23756	Bos taurus
21	314.4	70.8	786	4	BOVLSZ2DA	M26240	Bovine lyso
22	309.4	69.7	1020	4	BOVLSZM5A	L23757	Bos taurus
23	299.8	67.5	447	9	T0U76917	U76317	Trichyplithe
24	299.8	67.5	447	9	T0U76918	U76318	Trichyplithe
25	298.2	67.2	603	9	PELYSQC	X60235	P. entellus
26	296.6	66.8	447	9	CGU76916	U76316	Colobus que
27	293.6	66.1	1529	4	BOVLSZ01YM	L19980	Bos taurus
28	288.6	65.0	597	9	MMLYS	X6036	M. mulatta m
29	287	64.6	447	9	CTU76920	U76320	Cercopithec
30	285.4	64.3	447	9	PHU76919	U76319	Papio hamad
31	285.4	64.3	605	9	CELYS	X60237	C. aethiops
32	282.2	63.6	447	9	PU76914	U76914	Pongo pygma
33	280.6	63.2	447	9	PU76912	U76912	Pan troglod
34	280.6	63.2	1483	9	HOMLSZH	M19045	Human lysoz
35	280.6	63.2	1487	9	HOMLSZ	J03801	Human lysoz
36	280.6	63.2	1496	6	E01888	E01888	CDNA sequen
37	280.6	63.2	1496	6	E02193	E02193	DNA encodin
38	280.6	63.2	1507	9	BC0004147	BC0004147	Homo sapi
39	280.6	63.1	447	9	SCU76921	U76921	Saliniri sci
40	279	62.8	447	9	GGU76913	U76913	Gorilla gor
41	279	62.8	748	6	AX337938	M23119	Human lysoz
42	279	62.8	748	6	HOMLSZA	U76923	Callithrix
43	275.4	62.1	447	9	CU76922	U76922	Saguinus oe
44	275.4	62.0	447	9	CU76922	U76922	Saguinus oe
45	274.2	61.8	456	9	HSU2677	U25677	Homo sapien

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BASE COUNT	132 a 89 c 119 g 119 t	
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Query Match	100.0%; Score 444; DB 6; Length 459;	
Best Local Similarity	100.0%; Pred. No. 1.5e-111;	
Matches 444; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
OY	1 ATGAGGCGCTCGCTATTCTCGGGGTTTCTCTTCCTTCCTTCGTCGCTGCCAAGCAAGTC	60
DB	7 ATGAAAGGCTCTCGTTATTCCTGGGGTTTCTCTTCCTTCCTTCGTCGCTGCCAAGCAAGTC	66
OY	61 TTGAGAGATGTGACCTTCCGAGACTCTGAAGAAGTGGACCTGGACGGCTATAAGGA	120
DB	67 TTGAGAGATGTGACCTTCCGAGACTCTGAAGAAGTGGACCTGGACGGCTATAAGGA	126
OY	121 GTCAGCCTGGCAAACTGTTGTTGTTGACCAAGTGGAAAGCAAGTATTAACACAAAGCT	180
DB	127 GTCAGCCTGGCAAACTGTTGTTGTTGACCAAGTGGAAAGCAAGTATTAACACAAAGCT	186
OY	181 ACAAACTCAATTCCTAGCAGTGAAGAAAGCACTGATTTGGGATATTTCATATCAACAAAGCA	240
DB	187 ACAAACTCAATTCCTAGCAGTGAAGAAAGCACTGATTTGGGATATTTCATATCAACAAAGCA	246
OY	241 TGTGTGTATTAATGATGCCAAACCCCTTAATGACAGTGGAGCTGTATGATATTCCTGACG	300
DB	247 TGTGTGTATTAATGATGCCAAACCCCTTAATGACAGTGGAGCTGTATGATATTCCTGACG	306
OY	301 GAATTAATGAAAAATGACATCGCTAAACCTGTAGGGTGTGAAGCATATGTCAGTAG	360
DB	307 GAATTAATGAAAAATGACATCGCTTAACCTGTAGGGTGTGAAGCATATGTCAGTAG	366
OY	361 CAAGGCATTCACGCTGGGTGGCATGAAAAAGCATTTGTGCAGACCATGACGTGACAGT	420
DB	367 CAAGGCATTCACGCTGGGTGGCATGAAAAAGCATTTGTGCAGACCATGACGTGACAGT	426
OY	421 TACGTTGGAGGTTGCACCCCTGTAA 444	
DB	427 TACGTTGGAGGTTGCACCCCTGTAA 450	
RESULT 2		
BOVIS22B	951 bp	linear
LOCUS	BOVIS22B	951 bp
DEFINITION	Bovine lysozyme c isozyme 2b mRNA, complete cds.	MM 27-Apr-1993
ACCESSION	M26243 J04831 M27182	
VERSION	M26243.1 GI:163316	
KEYWORDS	lysozyme.	
SOURCE	Bovine abomasum, cDNA to mRNA, clone lambda-cBL[12,42].	
ORGANISM	Bos taurus	
REFERENCE	Emkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bos.	
AUTHORS	1 (bases 1 to 951)	
TITLE	Irwin,D.M. and Wilson,A.C.	
JOURNAL	Multiple cDNA sequences and the evolution of bovine stomach	
MEDLINE	lysosome	
PUBMED	J. Biol. Chem. 264 (19), 11387-11393 (1989)	
COMMENT	Draft entry and computer-readable sequence for [1] kindly submitted by D.M.Irwin, 23-JUN-1989.	
FEATURES	location/Qualifiers	
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	19. .462	
	/note="lysozyme 2b precursor"	
	/codon_start=1	
	/protein_id="AA30629.1"	
	/db_xref="GI:163317"	
	/translation="MKALVILGLFLFSVAVQGVFERCELARTLTKLGLDGKGVSLA	

	sig_peptide		19..72 /note="lysozyme 2b signal peptide"	
	mat_peptide		73..459 /product="Lysozyme 2b"	
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Query Match		100.0%;	Score 444;	DB 4; Length 951;
Best Local Similarity		100.0%;	Pred. No. 1.5e-111;	
Matches 444;	Conservative	0;	Mismatches	0; Indels 0; Gaps 0;
OY	1 ATGAAGGCGTCTGGATATTCTGGGGTTTCCTCCTTGCTGTGCCTGCCCAAGGCAAGGTC	60		
Dd	19 ATGAAGGCGTCTGGATATTCTGGGGTTTCCTCCTTGCTGTGCCTGCCCAAGGCAAGGTC	78		
OY	61 TTITGAGAGATGTGACCTTGCCAGAACTGTGAAGAAACTTGGACTGGACGCTATAAGGA	120		
Dd	79 TTTGAGAGATGTGACCTTGCCAGAACTGTGAAGAAACTTGGACTGGACGCTATAAGGA	138		
OY	121 GTCACCTTGGCAAACCTGGTGTGTTGGACAAGNGGGAAGCAAGTATTAACAAAAAAGCT	180		
Dd	139 GTCACCTTGGCAAACCTGGTGTGTTGGACAAGNGGGAAGCAAGTATTAACAAAAAAGCT	198		
OY	181 ACAAACTACAACTCTAGCAGTGAAAAGCACTGATTATGGAGATTTCAGATCAACAGCAA	240		
Dd	199 ACAAACTACAACTCTAGCAGTGAAAAGCACTGATTATGGAGATTTCAGATCAACAGCAA	258		
OY	241 TGGTGGTATANTANGCAAAACCCTTAATGCACTTGACGCTGTCAATATCCTGCAGC	300		
Dd	259 TGGTGGTATANTANGCAAAACCCTTAATGCACTTGACGCTGTCAATATCCTGCAGC	318		
OY	301 GAATTAAATGAAAAATGACATGCTAAAGCTTAGCGTGTGCGAACGATTTGTGCATGAG	360		
Dd	319 GAATTAAATGAAAAATGACATGCTAAAGCTTAGCGTGTGCGAACGATTTGTGCATGAG	378		
OY	361 CAAGCATATTACAGCTGGGTGGCATGCAAAAAGTCATTTGTGCAGACCATGACGTCAGAGT	420		
Dd	379 CAAAGCATATTACAGCTGGGTGGCATGCAAAAAGTCATTTGTGCAGACCATGACGTCAGAGT	438		
OY	421 TAGCTTGAGSGTTGCACCCGTGTA 444			
Dd	439 TAGCTTGAGSGTTGCACCCGTGTA 462			
RESULT 3				
BOVLZYMW7A		1060 bp	mRNA	linear MAY 10-MAR-1994
LOCUS	Bos taurus Lysozyme 7A mRNA.			
DEFINITION	L23758			
ACCESSION	L23758.1 GI:387905			
VERSION				
KEYWORDS	lysozyme.			
SOURCE	Bos taurus (cow).			
ORGANISM	Bos taurus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos. 1 (bases 1 to 1060) Takeuchi,K., Irwin,D.M., Gallup,M., Shindrot,E., Kai,H., Stewart,C.B. and Basbaum,C. Multiple cDNA sequences of bovine tracheal lysozyme J. Biol. Chem. 268 (36), 27440-27446 (1993)			
AUTHORS	J. Biol. Chem. 268 (36), 27440-27446 (1993)			
TITLE	94086565			
JOURNAL	8262986			
MEDLINE				
PUBMED				
FEATURES				
source	Location/Oualifiers			
	/organism="Bos taurus" /db_xref="taxon:9913" /cell_type="epithelial"/ gland" /tissue_type="trachea" /dev_stage="adult"			
BASE COUNT	337 a	181 c	223 g	319 t

Db 61 GAGATGTGAGCTTCCGAGAACTGTGAAGAACTTGGACGTGACGGCTATTAAGGAGTCAG 120
 QY 126 CCTGCAAACTGGTGTGTTTGGACCAATGGGAAGCAAGTATTAACCAAAAGCTCAAA 185
 Db 121 CCTGCAAACTGGTGTGTTTGGACCAATGGGAAGCAAGTATTAACCAAAAGCTCAAA 180
 QY 186 CTACATCTCAGCAGTGAAGCACTGATTAATGGATATTTTCAGATCAACAGCAATGCTG 245
 Db 181 CTACATCTCAGCAGTGAAGCACTGATTAATGGATATTTTCAGATCAACAGCAATGCTG 240
 QY 246 GTGTAATGATGGCAAAACCCCTAATGACATGACGGCTGCATGATCTCCGACGCAAT 305
 Db 241 GTGTAATGATGGCAAAACCCCTAATGACATGACGGCTGCATGATCTCCGACGCAAT 300
 QY 306 AATGAAATGACATGCTAAGCTGAGCTGTCGAACATATTTGTCAGTACGACGCAAG 365
 Db 301 AATGAAATGACATGCTAAGCTGAGCTGTCGAACATATTTGTCAGTACGACGCAAG 360
 QY 366 CATTACAGCTGGGTGGCAGTGAAGAACTGATTCGAGACCATGACGTGACAGTACGT 425
 Db 361 CATTACAGCTGGGTGGCAGTGAAGAACTGATTCGAGACCATGACGTGACAGTACGT 420
 QY 426 TGAGGGTTGCACCTGTAA 444
 Db 421 TGAGGGTTGCACCTGTAA 439
 RESULT 6
 109315 963 bp DNA linear PAT 02-DEC-1994
 LOCUS Sequence 1 from Patent WO 8904320.
 DEFINITION 109315
 ACCESSION 109315.1 GI:587976
 VERSION 109315.1 GI:587976
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 963)
 AUTHORS Digan, M.E., Harpold, M.M., Lair, S.V., Thill, G.P., Siegel, R.S., Ellis, S.B. and Williams, M.E.
 TITLE PRODUCTION OF ANIMAL LYSOZYME c VIA SECRETION FROM PICHIA PASTORIS AND COMPOSITION THEREFOR
 JOURNAL Patent: WO 8904320-A 1 18-MAY-1989;
 FEATURES
 source location/Qualifiers
 1..963
 /organism="unknown"
 BASE COUNT 298 a 165 c 200 g 299 t 1 others
 ORIGIN
 Query Match 98.5%; Score 437.4; DB 6; Length 963;
 Best Local Similarity 99.8%; Pred. No. 9,6e-110;
 Matches 438; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 306 AATGAAATGACATGCTAAGCTGTAGCGGTGCCAAAGCATATTGTCAAGGACGACG 365
 Db 324 AATGAAATGACATGCTAAGCTGTAGCGGTGCCAAAGCATATTGTCAAGGACGACG 383
 QY 366 CATTACAGCTGGGTGGCAGTGAAGAACTGATTCGAGACCATGACGTGACAGTACGT 425
 Db 384 CATTACAGCTGGGTGGCAGTGAAGAACTGATTCGAGACCATGACGTGACAGTACGT 443
 QY 426 TGAGGGTTGCACCTGTAA 444
 Db 444 TGAGGGTTGCACCTGTAA 462
 RESULT 7
 BOVLS23A
 LOCUS 1082 bp mRNA linear MAR 27-APR-1993
 DEFINITION Bovine lysozyme c isozyne 3a mRNA, complete cds.
 ACCESSION M26242 J04831 M27180
 VERSION M26242.1 GI:163322
 KEYWORDS
 SOURCE Lysozyme.
 ORGANISM Bovine abomasum, cDNA to mRNA, clone lambda-cbl[26,28].
 Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea; Bovidae; Bovinae; Bos.
 REFERENCE 1 (bases 1 to 1082)
 AUTHORS Irwin, D.M. and Wilson, A.C.
 TITLE Multiple cDNA sequences and the evolution of bovine stomach lysozyme
 JOURNAL J. Biol. Chem. 264 (19), 11387-11393 (1989)
 MEDLINE 89291894
 PUBMED 2738070
 COMMENT Draft entry and computer-readable sequence for [1] kindly submitted by D.M. Irwin, 23-JUN-1989
 FEATURES
 source location/Qualifiers
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 Query Match 96.0%; Score 426.4; DB 4; Length 1082;
 Best Local Similarity 97.5%; Pred. No. 1e-106;
 Matches 433; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 241 TGGTGTGTAATGATGAGCAAAACCCCTAATGACGTGAGCGGCTGCATGATCCGACG 300
 DB 249 TGGTGTGTAATGATGAGCAAAACCCCTAATGACGTGAGCGGCTGCATGATCCGACG 308
 QY 301 GAATTAATGAAATGACATGCTAAAGCTGTAGCGTGTGCAAAAGCATATTTGTACAGT 360
 DB 309 GAATTAATGAAATGACATGCTAAAGCTGTAGCGTGTGCAAAAGCATATTTGTACAGT 368
 QY 361 CAAGCATTTACAGCTGGTGGCATGAGAAAGTCTATTTGTGAGACCATGAGTACAGT 420
 DB 369 CAAGCATTTACAGCTGGTGGCATGAGAAAGTCTATTTGTGAGACCATGAGTACAGT 428
 QY 421 TACGTTGAGGGTTGACACCTGTAA 444
 DB 429 TATGTTCAAGGTTGACACCTGTAA 452

RESULT 8

BOVLS21B

LOCUS BOVLS21B 891 bp mRNA linear MAM 27-APR-1993
 DEFINITION Bovine lysozyme c isozyme 1b mRNA, complete cds.
 ACCESSION M26246 J04831 M27179
 VERSION M26246.1 GI:163312
 KEYWORDS lysozyme.
 SOURCE Bovine abomasum, cDNA to mRNA, clones lambda-cBL[3,4,35].
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.
 1 (bases 1 to 891)
 Irwin,D.M. and Wilson,A.C.
 Multiple cDNA sequences and the evolution of bovine stomach
 lysozyme
 J. Biol. Chem. 264 (19), 11387-11393 (1989)
 MEDLINE 89291894
 PUBMED 2738070

REFERENCE
 AUTHORS Irwin,D.M. and Wilson,A.C.
 TITLE Multiple cDNA sequences and the evolution of bovine stomach
 lysozyme
 J. Biol. Chem. 264 (19), 11387-11393 (1989)
 MEDLINE 89291894
 PUBMED 2738070
 COMMENT Draft entry and computer-readable sequence for [1] kindly submitted
 by D.M.Irwin, 23-JUN-1989.

FEATURES

Location/Qualifiers

source 1..891
 /organism="Bos taurus"
 /db_xref="taxon:9913"
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 mat_peptide 274 a 152 c 196 g 269 t

BASE COUNT 274 a 152 c 196 g 269 t
 ORIGIN
 Query Match 94.6%; Score 420; DB 4; Length 891;
 Best Local Similarity 96.6%; Pred. NO. 6e-105;
 Matches 429; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 ATGAAGGCTCTGCTATTTCTGAGGGTTCTCTTCTTCTGCTGCTGCCAAGCAAGTGC 60
 DB 8 ATGAAGGCTCTGCTATTTCTGAGGGTTCTCTTCTTCTGCTGCTGCCAAGCAAGTGC 67
 QY 61 TTTGAGAGATGAGCTGCTGCCAGACTCTGAAGAACTTGAGTGAAGGCTATTAAGGA 120
 DB 68 TTTGAGAGATGAGCTGCTGCCAGACTCTGAAGAACTTGAGTGAAGGCTATTAAGGA 127
 QY 121 GTGAGCTGGCAAACTGGTGTGTTGACCAATGGGAAAGCAAGTTATAACAAAGCT 180
 DB 128 GTGAGCTGGCAAACTGGTGTGTTGACCAATGGGAAAGCAAGTTATAACAAAGCT 187

QY 181 ACAACTACATCTTACAGTGAAGCACTGATTAATGAGATATTTGAGATCAACAGCAAA 240
 DB 188 ACAACTACATCTTACAGTGAAGCACTGATTAATGAGATATTTGAGATCAACAGCAAA 247
 QY 241 TGGTGTGTAATGATGAGCAAAACCCCTAATGACGTGAGCGGCTGCATGATCCGACG 300
 DB 248 TGGTGTGTAATGATGAGCAAAACCCCTAATGACGTGAGCGGCTGCATGATCCGACG 307
 QY 301 GAATTAATGAAATGACATGCTAAAGCTGTAGCGTGTGCAAAAGCATATTTGTACAGT 360
 DB 308 GAATTAATGAAATGACATGCTAAAGCTGTAGCGTGTGCAAAAGCATATTTGTACAGT 367
 QY 361 CAAGCATTTACAGCTGGTGGCATGAGAAAGTCTATTTGTGAGACCATGAGTACAGT 420
 DB 368 CAAGCATTTACAGCTGGTGGCATGAGAAAGTCTATTTGTGAGACCATGAGTACAGT 427
 QY 421 TACGTTGAGGGTTGACACCTGTAA 444
 DB 428 TATGTTGAGGGTTGACACCTGTAA 451

RESULT 9

BOVLS21A

LOCUS BOVLS21A 906 bp mRNA linear MAM 27-APR-1993
 DEFINITION Bovine lysozyme c isozyme 1a mRNA, complete cds.
 ACCESSION M26245 J04831 M27178
 VERSION M26245.1 GI:163310
 KEYWORDS lysozyme.
 SOURCE Bovine abomasum, cDNA to mRNA, clone lambda-cBL21.
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.
 1 (bases 1 to 906)
 Irwin,D.M. and Wilson,A.C.
 Multiple cDNA sequences and the evolution of bovine stomach
 lysozyme
 J. Biol. Chem. 264 (19), 11387-11393 (1989)
 MEDLINE 89291894
 PUBMED 2738070

REFERENCE
 AUTHORS Irwin,D.M. and Wilson,A.C.
 TITLE Multiple cDNA sequences and the evolution of bovine stomach
 lysozyme
 J. Biol. Chem. 264 (19), 11387-11393 (1989)
 MEDLINE 89291894
 PUBMED 2738070
 COMMENT Draft entry and computer-readable sequence for [1] kindly submitted
 by D.M.Irwin, 23-JUN-1989.

FEATURES

Location/Qualifiers

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 77..463
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BASE COUNT 276 a 155 c 198 g 277 t
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 Best Local Similarity 96.2%; Pred. NO. 4.6e-104;
 Matches 427; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1 ATGAAGGCTCTGCTATTTCTGAGGGTTCTCTTCTTCTGCTGCTGCCAAGCAAGTGC 60
 DB 23 ATGAAGGCTCTGCTATTTCTGAGGGTTCTCTTCTTCTGCTGCTGCCAAGCAAGTGC 82
 QY 61 TTTGAGAGATGAGCTGCTGCCAGACTCTGAAGAACTTGAGTGAAGGCTATTAAGGA 120
 DB 83 TTTGAGAGATGAGCTGCTGCCAGACTCTGAAGAACTTGAGTGAAGGCTATTAAGGA 142

QY 121 GTCAGCTGGCAAACTGTTGTGTGGACCAAAATGGGAAAGCAGTTATTAACACAAAAGCT 180
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 DB 143 GTCAGCTGGCAAACTGTTGTGTGGACCAAAATGGGAAAGCAGTTATTAACACAAAAGCT 202
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 QY 181 ACAAACTACATCTTACAGTGAAGACATGATTATGGGATATTTCAGATCAACACAAA 240
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 DB 263 TGGTGTGTATATGATGGCAAAACCCCTAATGACGTTGACGCGTGTATGTTATCTGACG 322
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 DB 323 GAATTAATGGAATATGATGCTAAAGCTGTAGCGTGTGCAAGCATATTGTCACTGAG 382
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 DB 383 CAAGGCAATTACAGCTGGTGGTGGCATGGAAGTCAATGTCAGACCATGACGTCAGCAGT 442
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 QY 421 TACGTTGAGGGTGGACCTGTATA 444
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 DB 443 TATGTTGAGGGTGGACCTGTATA 466
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RESULT 10
 BOVLS22C 877 bp mRNA linear MAM 27-APR-1993
 LOCUS
 DEFINITION Bovine lysozyme c lysozyme 2c mRNA, complete cds.
 ACCESSION M26244 J04831 M27183
 VERSION M26244.1 GI:163318
 KEYWORDS
 SOURCE Lysozyme.
 ORGANISM Bovine abomasum, CDNA to mRNA, clones lambda-cbl[20,36,39].
 Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.
 1 (bases 1 to 877)
 Irwin,D.M. and Wilson,A.C.
 Multiple cDNA sequences and the evolution of bovine stomach
 lysozyme
 J. Biol. Chem. 264 (19), 11387-11393 (1989)
 MEDLINE 89291894
 PUBMED 2738070

COMMENT
 Draft entry and computer-readable sequence for [1] kindly submitted
 by D.M.Irwin, 23-JUN-1989.

FEATURES
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 location/Qualifiers
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CDS
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 /db_xref="taxon:9913"
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 /note="Lysozyme 2c precursor"
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 VSEGSITAMVAKSHCRHDVSSYVEGCTL"
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 /note="Lysozyme 2c signal peptide"
 /product="Lysozyme 2c"
 /product="Lysozyme 2c"
 10..396
 /product="Lysozyme 2c"
 142 c 181 g 269 t

sig_peptide
 mat_peptide
 BASE COUNT 285 a 142 c 181 g 269 t
 ORIGIN

Query Match 89.5%; Score 397.4; DB 4; Length 877;
 Best Local Similarity 99.7%; Pred. No. 1e-98;
 Matches 398; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 46 GTCCAAAGCAAGCTTTGAGAGATGAGCTGCCAACAACCTGCAACAACTGGAGCTG 105
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QY 106 GACGGCTATAGGAGATGACCTGGCAAACTGTTGTGTGGACCAAAATGGGAAAGCAGT 165
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 DB 61 GACGGCTATAGGAGATGACCTGGCAAACTGTTGTGTGGACCAAAATGGGAAAGCAGT 120
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 QY 166 TATTAACAAAAGCTTACAACTACATCTTACAGTGAAGACATGATTATGGATATT 225
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 DB 121 TATTAACAAAAGCTTACAACTACATCTTACAGTGAAGACATGATTATGGATATT 180
 |||||
 QY 226 CAGATCAACAGCAATGGGTTGATATATGCAAAACCCCTAATGCACTGACGCGT 285
 |||||
 DB 181 CAGATCAACAGCAATGGGTTGATATATGCAAAACCCCTAATGCACTGACGCGT 240
 |||||
 QY 286 CATGATCTCTGACGCAATTAATGGAATATGACATGCTTAAAGCTGTAGCGTGAAG 345
 |||||
 DB 241 CATGATCTCTGACGCAATTAATGGAATATGACATGCTTAAAGCTGTAGCGTGAAG 300
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 QY 346 CATATGTCAGTACGACCAAGCATTTACACCTGGTGGTGGCATGGAAGTCACTGTCAGAC 405
 |||||
 DB 301 CATATGTCAGTACGACCAAGCATTTACACCTGGTGGTGGCATGGAAGTCACTGTCAGAC 360
 |||||
 QY 406 CATGACGTCAGCAGTTACGTTGAGGGTGGACCCCTGTAA 444
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 DB 361 CATGACGTCAGCAGTTACGTTGAGGGTGGACCCCTGTAA 399
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RESULT 11
 SHPLZM3A 875 bp mRNA linear MAM 27-APR-1993
 LOCUS
 DEFINITION Sheep lysozyme 3a (lyz3a) mRNA, complete cds.
 ACCESSION M32496 J05279
 VERSION M32496.1 GI:165971
 KEYWORDS
 SOURCE Lysozyme 3a.
 ORGANISM Sheep abomasum, CDNA to mRNA.
 Ovis aries
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Caprinae; Ovis.
 1 (bases 1 to 875)
 Irwin,D.M. and Wilson,A.C.
 Concerted evolution of ruminant stomach lysozymes. Characterization
 of lysozyme cDNA clones from sheep and deer
 J. Biol. Chem. 265 (9), 4944-4952 (1990)
 MEDLINE 90202968
 PUBMED 2318875

COMMENT
 Draft entry and computer-readable sequence for [1] kindly submitted
 by D.M.Irwin, 01-MAR-1990.

FEATURES
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 location/Qualifiers
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 1..387
 /product="Lysozyme 3a"
 1..17
 /note="PCR primer"
 148 c 189 g 260 t

mat_peptide
 misc_feature
 BASE COUNT 278 a 148 c 189 g 260 t
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Query Match 82.8%; Score 367.6; DB 4; Length 875;
 Best Local Similarity 96.4%; Pred. No. 1.6e-90;
 Matches 376; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 55 AAGGCTTTGAGAGATGAGCTTGCAGAACTCTGAAGAACTGAGCTGACGCGCTAT 114
 |||||
 DB 1 AAGGCTTTGAGAGATGAGCTTGCAGAACTCTGAAGAACTGAGCTGACGCGCTAT 60
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QY 115 AAGGAGTCAGCCTGGCAAACTGTTGTTGTTGACCAATGGGAAGCATTATACACA 174
|||||
DB 61 AAGGAGTCAGCCTGGCAAACTGTTGTTGTTGACCAATGGGAAGCATTATACACA 120
QY 175 AAAGCTACAACTACAACTCTAGCAGTGAAGCAGCTATTTATGGATTTTCAGATCAC 234
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DB 121 AAAGCTACAACTACAACTCTAGCAGTGAAGCAGCTATTTATGGATTTTCAGATCAC 180
QY 235 AGCAATAGTGTGTTAATGATGACCAAAACCCCTAATGAGTGAAGCAGCTGATATTC 294
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DB 181 AGCAATAGTGTGTTAATGATGACCAAAACCCCTAATGAGTGAAGCAGCTGATATTC 240
QY 295 TGCAGCAATTAATGAAATAATGACATCGCTAAGCTGTAGCGGTGTGCAAGCATATTGTC 354
|||||
DB 241 TGCAGCAATTAATGAAATAATGACATCGCTAAGCTGTAGCGGTGTGCAAGCATATTGTC 300
QY 355 AGTGAGCAAGGCAATTAACAGCTGGGTGGCATGGAAGATGATTTGAGACCATGACGTC 414
|||||
DB 301 AGTGAGCAAGGCAATTAACAGCTGGGTGGCATGGAAGATGATTTGAGACCATGACGTC 360
QY 415 AGCAGTTACGTTGAGGGTTGCACCCCTGTAA 444
|||||
DB 361 AGCAGTTACGTTGAGGGTTGCACCCCTGTAA 390

RESULT 12

LOCUS SHPLZM1B 881 bp mRNA linear MAM 27-Apr-1993
DEFINITION Sheep lysozyme 1b (12mb) mRNA, 3' end.
ACCESSION M32493 J05279
VERSION M32493.1 GI:165965
KEYWORDS lysozyme 1b.
SOURCE Sheep abomasum, cDNA to mRNA.
ORGANISM Ovis aries

REFERENCE
AUTHORS 1 (bases 1 to 881)
TITLE Irwin,D.M. and Wilson,A.C.
JOURNAL Concerted evolution of ruminant stomach lysozymes. Characterization
MEDLINE of lysozyme cDNA clones from sheep and deer
PUBMED J. Biol. Chem. 265 (9), 4944-4952 (1990)
90202968
2318875

COMMENT
Draft entry and computer-readable sequence for [1] kindly submitted
by D.M.Irwin, 01-MAR-1990.

FEATURES
source location/Qualifiers
1..881
/organism="Ovis aries"
/db_xref="taxon:9940"

CDS
1..390
/note="lysozyme 1b precursor"

mat_peptide
1..387
/product="lysozyme 1b"
misc_feature
1..17
/note="PCR primer"

BASE COUNT 285 a 145 c 182 g 269 t
ORIGIN

Query Match 82.8%; Score 367.6; DB 4; Length 881;
Best Local Similarity 96.4%; Pred. No. 1.6e-90;
Matches 376; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 55 AAGGCTTTGAGAGATGAGCTTGCAGAACTCGAAGAACTGGAGTGGAGCGCTAT 114
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DB 1 AAGGCTTTGAGAGATGAGCTTGCAGAACTCGAAGAACTGGAGTGGAGCGCTAT 60

QY 115 AAGGAGTCAGCCTGGCAAACTGTTGTTGTTGACCAATGGGAAGCATTATACACA 174
|||||
DB 61 AAGGAGTCAGCCTGGCAAACTGTTGTTGTTGACCAATGGGAAGCATTATACACA 120
QY 175 AAAGCTACAACTACAACTCTAGCAGTGAAGCAGCTATTTATGGATTTTCAGATCAC 234
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DB 121 AAAGCTACAACTACAACTCTAGCAGTGAAGCAGCTATTTATGGATTTTCAGATCAC 180
QY 235 AGCAATAGTGTGTTAATGATGACCAAAACCCCTAATGAGTGAAGCAGCTGATATTC 294
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DB 181 AGCAATAGTGTGTTAATGATGACCAAAACCCCTAATGAGTGAAGCAGCTGATATTC 240
QY 295 TGCAGCAATTAATGAAATAATGACATCGCTAAGCTGTAGCGGTGTGCAAGCATATTGTC 354
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DB 241 TGCAGCAATTAATGAAATAATGACATCGCTAAGCTGTAGCGGTGTGCAAGCATATTGTC 300
QY 355 AGTGAGCAAGGCAATTAACAGCTGGGTGGCATGGAAGATGATTTGAGACCATGACGTC 414
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DB 301 AGTGAGCAAGGCAATTAACAGCTGGGTGGCATGGAAGATGATTTGAGACCATGACGTC 360
QY 415 AGCAGTTACGTTGAGGGTTGCACCCCTGTAA 444
|||||
DB 361 AGCAGTTACGTTGAGGGTTGCACCCCTGTAA 390

RESULT 13

LOCUS SHPLZM1C 881 bp mRNA linear MAM 27-Apr-1993
DEFINITION Sheep lysozyme 1c (12lc) mRNA, 3' end.
ACCESSION M32494 J05279
VERSION M32494.1 GI:165967
KEYWORDS lysozyme 1c.
SOURCE Sheep abomasum, cDNA to mRNA.
ORGANISM Ovis aries

REFERENCE
AUTHORS 1 (bases 1 to 881)
TITLE Irwin,D.M. and Wilson,A.C.
JOURNAL Concerted evolution of ruminant stomach lysozymes. Characterization
MEDLINE of lysozyme cDNA clones from sheep and deer
PUBMED J. Biol. Chem. 265 (9), 4944-4952 (1990)
90202968
2318875

COMMENT
Draft entry and computer-readable sequence for [1] kindly submitted
by D.M.Irwin, 01-MAR-1990.

FEATURES
source location/Qualifiers
1..881
/organism="Ovis aries"
/db_xref="taxon:9940"

CDS
1..390
/note="lysozyme 1c precursor"

mat_peptide
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/product="lysozyme 1c"
misc_feature
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/note="PCR primer"

BASE COUNT 285 a 144 c 183 g 269 t
ORIGIN

Query Match 82.8%; Score 367.6; DB 4; Length 881;
Best Local Similarity 96.4%; Pred. No. 1.6e-90;
Matches 376; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 55 AAGGCTTTGAGAGATGAGCTTGCAGAACTCGAAGAACTGGAGTGGAGCGCTAT 114
|||||
DB 1 AAGGCTTTGAGAGATGAGCTTGCAGAACTCGAAGAACTGGAGTGGAGCGCTAT 60

QY 115 AAGGAGTCAGCCCTGGCAAACTGGTTGTGTTGACCAAAATGGCAAGCACTTAAACACA 174
|||||
Db 61 AAGGAGTCAGCCCTGGCAAACTGGTTGTGTTGACCAAAATGGCAAGCACTTAAACACA 120
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QY 175 AAGGCTCAAACTACATTCCTAGCAGTGAAGCAGCATGATGATGATTTTGCATGACAC 234
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Db 121 AAGGCTCAAACTACATTCCTAGCAGTGAAGCAGCATGATGATGATTTTGCATGACAC 180
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QY 235 AGCAATGTGTGTATATGATGAGCAAAACCCCTAATGAGTGAAGGCTGTCATGATGC 294
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QY 295 TGCAGCGAATTAATGGAATAATGACATGCTAAAGCTGTAGCGTGCAGACATATGTC 354
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QY 355 AGTGAGCAAGGATTAATGAGCGCTGGTGAGTGAAGAAAGTCATGTGAGACCATGACGTC 414
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Db 301 AGTGAGCAAGGATTAATGAGCGCTGGTGAGTGAAGAAAGTCATGTGAGACCATGACGTC 360
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QY 415 AGCAGTTACGTTGAGGCTTGACACCTGTAA 444
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Db 361 AGCAGTTACGTTGAGGCTTGACACCTGTAA 390
|||||

RESULT 14
SHP12M2A 881 bp mRNA linear MAM 27-APR-1993
LOCUS SHP12M2A
DEFINITION Sheep lysozyme 2a (lyz2a) mRNA, 3' end.
ACCESSION M32495 J05279
VERSION M32495.1 GI:165969
KEYWORDS lysozyme 2a.
SOURCE Sheep abomasum, cDNA to mRNA.
ORGANISM Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Caprinae; Ovis.
1 (bases 1 to 881)
Irwin,D.M. and Wilson,A.C.
Concerted evolution of ruminant stomach lysozymes. Characterization
of lysozyme cDNA clones from sheep and deer
J. Biol. Chem. 265 (9), 4944-4952 (1990)
90202968
PUBMED 2318875
COMMENT Draft entry and computer-readable sequence for [1] kindly submitted
by D.M.Irwin, 01-MAR-1990.
FEATURES
source location/Qualifiers
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/db_xref="taxon:9940"
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QGITAWVAMKSHCRDHVSSYVEGCTL"
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1..17
misc_feature /note="PCR primer"
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BASE COUNT 287 a 144 c 183 g 267 t
ORIGIN

Query Match 82.8%; Score 367.6; DB 4; Length 881;
Best Local Similarity 96.4%; Pred. No. 1.6e-90;
Matches 376; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 55 AAGGCTTTGAGAGATGAGCTTGCCAGAACTGTGAAGAACTTGAGTGAAGCGCTAT 114
|||||
Db 1 AAGGCTTTGAGAGATGAGCTTGCCAGAACTGTGAAGAACTTGAGTGAAGCGCTAT 60
|||||

QY 115 AAGGAGTCAGCCCTGGCAAACTGGTTGTGTTGACCAAAATGGCAAGCACTTAAACACA 174
|||||
Db 61 AAGGAGTCAGCCCTGGCAAACTGGTTGTGTTGACCAAAATGGCAAGCACTTAAACACA 120
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QY 175 AAGGCTCAAACTACATTCCTAGCAGTGAAGCAGCATGATGATGATTTTGCATGACAC 234
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QY 295 TGCAGCGAATTAATGGAATAATGACATGCTAAAGCTGTAGCGTGCAGACATATGTC 354
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Db 241 TGCAGCGAATTAATGGAATAATGACATGCTAAAGCTGTAGCGTGCAGACATATGTC 300
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QY 355 AGTGAGCAAGGATTAATGAGCGCTGGTGAGTGAAGAAAGTCATGTGAGACCATGACGTC 414
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Db 301 AGTGAGCAAGGATTAATGAGCGCTGGTGAGTGAAGAAAGTCATGTGAGACCATGACGTC 360
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QY 415 AGCAGTTACGTTGAGGCTTGACACCTGTAA 444
|||||
Db 361 AGCAGTTACGTTGAGGCTTGACACCTGTAA 390
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RESULT 15
SHP12M1A 881 bp mRNA linear MAM 27-APR-1993
LOCUS SHP12M1A
DEFINITION Sheep lysozyme 1a (lyz1a) mRNA, 3' end.
ACCESSION M32492 J05279
VERSION M32492.1 GI:165963
KEYWORDS lysozyme 1a.
SOURCE Sheep abomasum, cDNA to mRNA.
ORGANISM Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Caprinae; Ovis.
1 (bases 1 to 881)
Irwin,D.M. and Wilson,A.C.
Concerted evolution of ruminant stomach lysozymes. Characterization
of lysozyme cDNA clones from sheep and deer
J. Biol. Chem. 265 (9), 4944-4952 (1990)
90202968
PUBMED 2318875
COMMENT Draft entry and computer-readable sequence for [1] kindly submitted
by D.M.Irwin, 01-MAR-1990.
FEATURES
source location/Qualifiers
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<1..390
/note="lysozyme 1a precursor"
/codon_start=1
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YNPSESTDYGIQINSKMCNDKTPNAVDCVHSCSLMENNIAKAVACAHYSE
QGITAWVAMKSHCRDHVSSYVEGCTL"
1..387
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misc_feature /note="PCR primer"
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BASE COUNT 285 a 144 c 182 g 270 t
ORIGIN

Query Match 82.4%; Score 366; DB 4; Length 881;
Best Local Similarity 96.2%; Pred. No. 4.5e-90;
Matches 373; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 55 AAGGCTTTGAGAGATGAGCTTGCCAGAACTGTGAAGAACTTGAGTGAAGCGCTAT 114
|||||
Db 1 AAGGCTTTGAGAGATGAGCTTGCCAGAACTGTGAAGAACTTGAGTGAAGCGCTAT 60
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QY 115 AAGGAGTCAGCCTGGCAAACTGGTTGTTGACCAATGGGAAAAGCAGTTATAACACA 174
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Db 61 AAGGAGTCAGCCTGGCAAACTGGTTGTTGACCAATGGGAAAAGCAGTTATAACACA 120
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QY 175 AAAGCTACAACCTACAACTCTAGCAGTGAAGCACTGATTATGGATATTTGAGATCAAC 234
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QY 295 TGCAGCGAATTAATGGAATGACATCGCTAAAGCTAGCGTGTGCAAGCATATTGTC 354
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QY 355 AGTGACCAAGGCATTACAGCTGGGTGGCATGGAAAAGTCATTGTGAGACCATGACGTC 414
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Db 301 AGTGACCAAGGCATTACAGCTGGGTGGCATGGAAAAGTCATTGTGAGACCATGACGTC 360
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QY 415 AGCAGTTACGTTGAGGGTTGCACCCCTGTAA 444
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Db 361 AGCAGTTACGTTGAGGGTTGCACCCCTGTAA 390
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Search completed: July 5, 2003, 06:13:47
Job time : 1383 secs

	XX	Doane G.	Wellichko S.
	DT		

Human macrophage-e
DNA encoding novel
Sequence encoding
Pancreas cancer re
Sequence encoding
Sequence of human
Sequence encoding
Human colon tumour
Human lung-specific
Human macrophage-e
DNA encoding novel
Human colon cancer
Sequence encoding
Nucleotide sequence
Synthetic human ly
Human colon tumour
Synthetic human ly
Human lysozyme DNA
Avtan lysozyme stig
Mutant human lysoz
Human lysozyme cod
Sequence of synthe
Human lung tumour
Sequence of natura
Human lysozyme gen
Human lysozyme H
Sequence encoding
Synthetic human ly
Sequence of Taq I-
Sequence encoding
Modified DNA sequ
Sequence of the Ta
TaqI - XhoI fragmen
pRIILy-2 human lyc
Human colon cancer
Mutant human lysoz

XX	04-Oct-2002	(first entry)
DT		
XX	p1044-Bolys plasmid DNA.	
DE		
XX	Bovine; viral vector; transgenic plant; lysozyme; antibacterial;	
KW	Pierce's disease; PD; Xylella fastidiosa bacterium infection;	
KM	anti-Xylella reagent; grapevine; cyclic; circular; gene; ds.	
XX		
OS	Chimeric - Bos sp.	
OS	Chimeric - Unidentified.	
XX		
FH	Key	Location/Qualifiers
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FT		/note= "Bovine lysozyme DNA"
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PN	WO200233041-A2.	
XX		
PD	25-Apr-2002.	
XX		
PF	17-Oct-2001; 2001WO-US32147.	
XX		
PR	18-Oct-2000; 2000US-240967P.	
XX		
PA	(IARG-) LARGE SCALE BIOLOGY CORP.	
XX		
PI	Pogue G, Velichko S;	
XX		
DR	WPI: 2002-479667/51.	
XX		
PT	Producing bovine lysozyme (Bolys) in plants e.g. grapevines, useful for	
PT	protecting grapevines against Pierce's disease by infecting host plant	
PT	with recombinant virus containing nucleic acid encoding Bolys -	
XX		
PS	Claim 3; Fig 2; 36pp. English.	
XX		
CC	The invention relates to viral vectors and methods for producing	
CC	transgenic plants that express heterologous DNA that encode a	
CC	riantgenic lysozyme, preferably bovine. This lysozyme protects against	
CC	diseases caused by plant pathogens particularly bacterial pathogens.	
CC	The method is useful for producing bovine lysozyme in host plants e.g.	
CC	grapevines. Plasmid encoding a recombinant plant virus which comprises	
CC	a bovine lysozyme encoding nucleic acid, is useful for producing bovine	
CC	lysozyme in a plant. It is also useful for producing bovine lysozyme	
CC	protein which acts as an anti-Xylella reagent for development of a	
CC	recombinant source of Bolys protein for treating grapevines against	
CC	Pierce's disease (PD). The method is useful for protecting grapevines	
CC	against Xylella fastidiosa bacterium infection that causes PD. The	
CC	present sequence is p1044-Bolys plasmid DNA containing bovine lysozyme	
CC	DNA.	
XX		
SQ	Sequence 10130 BP; 2854 A; 2078 C; 2492 G; 2706 T; 0 other;	
XX		
Query Match	100.0%; Score 444; DB 24; Length 10130;	
Best Local Similarity	100.0%; Pred. No. 1,2e-126;	
Matches 444; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
OY	1 ATGAAGCTCTCGTATTATTCGTGGGTTTCTCTCCTTCCTTGTCGCTGTCCAAGCAAGTGC 60	
DB	5767 ATGAAGCTCTCGTATTATTCGTGGGTTTCTCTCCTTCCTTGTCGCTGTCCAAGCAAGTGC 5826	
OY	61 TTGAGACATGTGAGCTTGCCAGAACCTGTGAAGAACAATGGACTGGACGGGTATAAAGGA 120	
DB	5827 TTGAGACATGTGAGCTTGCCAGAACCTGTGAAGAACAATGGACTGGACGGGTATAAAGGA 5886	
OY	121 GTCAAGCTTGCAAACTGGTTGTGTTTGACCAATATGGGAAGCAAGTTATTAACAAAAGCT 180	
DB	5887 GTCAAGCTTGCAAACTGGTTGTGTTTGACCAATATGGGAAGCAAGTTATTAACAAAAGCT 5946	
OY	181 ACAAACTCAATCCAGACAGTGAAGAAAGCATATTTGGGATATTTCAATCAACAGCAA 240	
DB	5947 ACAAACTCAATCCAGACAGTGAAGAAAGCATATTTGGGATATTTCAATCAACAGCAA 6006	

OY		241	TGGGCGGTATGATGATGGCAAAACCCCTAATGCATTGAGCGGCTGTCATGTAATCCTGACG	300
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Db		6067	GAATTATATGGAATAATGACATCGCTAAAGCTGTAGCGTGTCGAAAGCATATTGTCAGTGAG	6126
OY		361	CMAAGCATTTACAGCCTTGSGGTGGCATGGAANAAGTATTGTGCAGACCATGACGTAGACGT	420
Db		6127	CMAAGCATTTACAGCCTTGSGGTGGCATGGAANAAGTATTGTGCAGACCATGACGTAGACGT	6186
OY		421	TACSTTGAGGSGTTCACCCCTGTAA	444
Db		6187	TACSTTGAGGSGTTCACCCCTGTAA	6210
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RESULT 4				
ID	AAV08922	AAV08922 standard; cDNA; 964 BP.		
XX	AAV08922;			
XX	AC			
XX	DT	26-FEB-1999 (first entry)		
XX	DE	Bovine Lysozyme c2 protein coding sequence.		
XX	KW	Lysozyme; signal peptide; transgenic plant; plant pathogen;		
XX	RW	pathogen resistance; ds.		
XX	OS	Bos sp.		
XX	Key	Location/Qualifiers		
FT	CDS	25..462		
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XX	US5850025-A.			
PX	PD	15-DEC-1998.		
XX	PE	22-APR-1997; 97US-0919093.		
PX	PR	12-JAN-1995; 95US-0373390.		
PX	PR	19-SEP-1991; 91US-0762679.		
PX	PR	25-NOV-1991; 91US-0798223.		
PR	22-APR-1997; 97US-0919093.			
XX	PA	(SIBI-) SIBIA NEUROSCIENCES INC.		
XX	PI	Fitzmaurice LC, Mirkov TE;		
XX	DR	WPI; 1999-069855/06.		
XX	DR	P-PSDB; AAW73502.		
XX	PT	Transgenic plants resistant to bacterial pathogens - contain		
XX	PT	ruminant Lysozyme gene		
XX	PS	Example 1; Column 37-40; 23pp; English.		
XX	CC	This sequence encodes the bovine lysozyme c2 and can be		
XX	CC	used in the transgenic plant of the invention. The transgenic plant is		
XX	CC	resistant to plant pathogens and contains heterologous DNA encoding a		
XX	CC	ruminant or ruminant-like lysozyme, the plant expresses sufficient levels		
XX	CC	of the lysozyme to render it less susceptible to the pathogens than the		
XX	CC	wild-type plant. The plants are resistant to bacterial pathogens such as		
XX	CC	Pseudomonas syringae or Erwinia carotovora.		
XX	SQ	Sequence 964 BP; 297 A; 165 C; 201 G; 301 T; 0 other;		
<hr/>				
Query Match	98.9%; Score 439; DB 20; Length 964;			
Best Local Similarity	100.0%; Pred. NO. 1.6e-125; Mismatches 0; Indels 0; Gaps 0;			
Matches 439; Conservative	0; Mismatches 0; Indels 0; Gaps 0;			

QY 61 TTGAGAGATGTAGCTGGCAGAACTGTGAGAACTTGAGCTGAGCGCTATTAAGGA 120
 Db 74 TTTGAAAGGTGTAGTTGGCCAGAACTGTGAAAGATTGGGAATGATGGCTACAGGGGA 133
 QY 121 GTGAGCGTGGCAAACTGGTGTGTTGACCAATGGGAAAGCACTTATTAACAAAAAGCT 180
 Db 134 ATCAGCGCTAGCAAACTGGATGTGTTGGCCAAATGGAGAGTGTTCACACACAGAGCT 193
 QY 181 ACAAACTACATCTTACAGTGAAGCACTGATTTATGATTTTTCAGATCAACAGCAAA 240
 Db 194 ACAAACTACATCTTACAGTGAAGCACTGATTTATGATTTTTCAGATCAACAGAGCT 253
 QY 241 TGTGGTGTATGATGCGCAAAACCCCTAATGACAGTTCAGCTGATATCTCCAGC 300
 Db 254 TACTGTGTATGATGCGCAAAACCCCTAATGACAGTTCAGCTGATATCTCCAGCT 313
 QY 301 GAATTAATGAAATGACATGCTAAAGCTGAGCGTGTGCAAAAGCATATTGTCAGTA- 359
 Db 314 GCTTGTGCTGAAAGTAACTGATGCTGATGCTGTGTCGCAAAAGAGGGTTCGCGTAT 373
 QY 360 --GCAAGGCAATACAGCTGGTGGCATGAGAAAAGTCATTTGCGAGCCATGACGTCAGC 417
 Db 374 CCACAAGGCAATTAAGAGCATGGGTGGCATGAGAAAATCGTTGTCAAAACAGAGATGTCGGT 433
 QY 418 AGTTACGTTGAGGGTTCACCCCTGTAA 444
 Db 434 CAGTATGTTCAAGGTGTGGAGTGTAA 460
 RESULT 8
 ID AAO03369 standard; DNA; 1494 BP.
 AC AAO03369;
 XX 20-DEC-1990 (first entry)
 DT
 DE Sequence encoding human lysozyme.
 XX
 KW Transgenic animal; enzyme; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT sig_peptide 14..67
 FT mat_peptide 68..460
 FT /*tag= a
 FT /*tag= b
 XX JP02005879-A.
 PN
 XX 10-JAN-1990.
 PD
 XX 21-JUN-1988; 88JP-0151106.
 PF
 XX 21-JUN-1988; 88JP-0151106.
 PR
 XX (TAKE) TAKEDA CHEMICAL IND KK.
 PA WPI; 1990-053916/08.
 DR P-PSDB; AAR06108.
 XX
 PT Human lysozyme gene -
 XX useful promoter for genetic expression of animal culturing cell
 PS ; Fig 4-1 to 4-3 Pages 834-835; 13pp; Japanese.
 XX
 CC Human lysozyme DNA can be used to obtain transgenic animals, e.g. mice.
 CC It can also be produced by culturing animal cells, and it can
 CC promote the genetic expression of these animal cells.
 XX
 XX Sequence 1494 BP; 441 A; 298 C; 309 G; 446 T; 0 other;

Query Match 63.2%; Score 280.6; DB 11; Length 1494;
 Best Local Similarity 78.3%; Pred. No. 1.8e-76;
 Matches 350; Conservative 0; Mismatches 94; Indels 3; Gaps 1;
 QY 1 ATGAGGCTCTGCTGTTATTTCTGGGGTTTCTCTTCTTCTGCTGCTGCAAGCAAGGTC 60
 Db 14 ATGAGGCTCTGCTGTTATTTCTGGGGTTTCTCTTCTTCTGCTGCTGCAAGCAAGGTC 73
 QY 61 TTTGAGAGTGTGAGCTGGCCAGAACTGTGAGAACTTGAGCTGAGCGCTATTAAGGA 120
 Db 74 TTTGAAAGGTGTAGTTGGCCAGAACTGTGAAAGATTGGGAATGATGGCTACAGGGGA 133
 QY 121 GTGAGCGTGGCAAACTGGTGTGTTGACCAATGGGAAAGCACTTATTAACAAAAAGCT 180
 Db 134 ATCAGCGCTAGCAAACTGGATGTGTTGGCCAAATGGAGAGTGTTCACACACAGAGCT 193
 QY 181 ACAAACTACATCTTACAGTGAAGCACTGATTTATGATTTTTCAGATCAACAGCAAA 240
 Db 194 ACAAACTACATCTTACAGTGAAGCACTGATTTATGATTTTTCAGATCAACAGAGCT 253
 QY 241 TGTGGTGTATGATGCGCAAAACCCCTAATGACAGTTCAGCTGATATCTCCAGC 300
 Db 254 TACTGTGTATGATGCGCAAAACCCCTAATGACAGTTCAGCTGATATCTCCAGCT 313
 QY 301 GAATTAATGAAATGACATGCTAAAGCTGAGCGTGTGCAAAAGCATATTGTCAGTA- 359
 Db 314 GCTTGTGCTGAAAGTAACTGATGCTGATGCTGTGTCGCAAAAGAGGGTTCGCGTAT 373
 QY 360 --GCAAGGCAATACAGCTGGTGGCATGAGAAAAGTCATTTGCGAGCCATGACGTCAGC 417
 Db 374 CCACAAGGCAATTAAGAGCATGGGTGGCATGAGAAAATCGTTGTCAAAACAGAGATGTCGGT 433
 QY 418 AGTTACGTTGAGGGTTCACCCCTGTAA 444
 Db 434 CAGTATGTTCAAGGTGTGGAGTGTAA 460
 RESULT 9
 ID AAN92386 standard; DNA; 1496 BP.
 AC AAN92386;
 XX 03-JUN-1990 (first entry)
 DT
 DE DNA coding for the signal peptide and mature protein of human lysozyme
 DE (HL).
 XX
 KW Human lysozyme; HL; bacterial infection.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT sig_peptide 14..67
 FT mat_peptide 68..457
 FT /*tag= a
 FT /*tag= b
 FT CDS 14..460
 FT /*tag= c
 XX JP01074989-A.
 PN
 XX 20-MAR-1989.
 PD
 XX 16-SEP-1987; 87JP-0229752.
 PF
 XX 16-SEP-1987; 87JP-0229752.
 PR
 XX (TAKE) TAKEDA CHEMICAL IND KK.
 PA WPI; 1989-127529/17.
 DR P-PSDB; AAP93510.
 XX

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	YY	18	ACAACTACAATCCGTGCGTGAAGCACTGATTATGGATTTTCAGATTACACGAAA	240
	Dd	279	ACAACTACAATGCCTGGAGACAGCAAAGCACTGATTATGGGATTTTTCAGATCAATAAGGCC	338
OY		241	TGGTGSTGTAATGATGAGCAAAACCCTAATGCAATGACGGCTGCTGATTCCTGCAGC	3000
	Dd	339	TACTGSGTAAATGATGGCAAAACCCCAGAGCATTAATGCTCTGCATTATCCTGCAGT	398
OY		301	GAAITTAATGAAAAATGACATTCCTTAAGCTGTAGCGGTGTCGAAAACATATTGTCAGTA-	35
	Dd	399	GCTTTCCTSCAAAGATAAACATCCGATGCTGTAGCTTGCAAAAGAAGGGTTGCTCGTAT	458
OY		360	--GCAAGGATTACACGCTGGGTGGCATGGAATGATCTTGCAGACATGACGTACAGC	417
Dd		459	CCCAAGGCGATTTAGACATAGGCTGGCATGAGAAATCTGTGTCAAAACAGAGATGTCCGT	518
OY		418	AGTTAACGTTGAGGGTTGCACCCCTGPA	444
Dd		519	CAGTATGTTCAAGGTTGTGGAGTAPA	545
 RESULT_13 ABL70110 ID ABL70110 standard; DNA: 748 BP.				
XX	AC	ABL70110;		
XX	DT	15-MAY-2002 (first entry)		
DE		Pancreas cancer related gene sequence SEQ ID NO:8447.		
KX	Homo sapiens.			
WM	stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;			
KW	cytostatic; gene therapy; anti-neoplastic; Wilms tumour; adenocarcinoma;			
XK	gene; ds.			
XX				
OS				
PN	MO200194629-A2.			
PD	13-DEC-2001.			
PE	30-MAY-2001; 2001WO-US10838.			
PR	05-JUN-2000; 2000US-209473P.			
PR	05-JUN-2000; 2000US-209531P.			
PR	18-SEP-2000; 2000US-23133P.			
PR	18-SEP-2000; 2000US-233617P.			
PR	20-SEP-2000; 2000US-234009P.			
PR	20-SEP-2000; 2000US-234034P.			
PR	20-SEP-2000; 2000US-234052P.			
PR	22-SEP-2000; 2000US-234509P.			
PR	22-SEP-2000; 2000US-234567P.			
PR	25-SEP-2000; 2000US-234923P.			
PR	25-SEP-2000; 2000US-234924P.			
PR	25-SEP-2000; 2000US-235077P.			
PR	25-SEP-2000; 2000US-235082P.			
PR	25-SEP-2000; 2000US-235134P.			
PR	25-SEP-2000; 2000US-235280P.			
PR	26-SEP-2000; 2000US-235637P.			
PR	26-SEP-2000; 2000US-235638P.			
PR	27-SEP-2000; 2000US-235711P.			
PR	27-SEP-2000; 2000US-235720P.			
PR	27-SEP-2000; 2000US-235840P.			
PR	27-SEP-2000; 2000US-235863P.			
PR	28-SEP-2000; 2000US-236028P.			
PR	28-SEP-2000; 2000US-236032P.			
PR	28-SEP-2000; 2000US-236033P.			
PR	28-SEP-2000; 2000US-236034P.			
PR	28-SEP-2000; 2000US-236109P.			
PR	28-SEP-2000; 2000US-236112P.			
PR	29-SEP-2000; 2000US-236842P.			
PR	29-SEP-2000; 2000US-236891P.			

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Run on:      July  5, 2003, 05:03:49 ; Search time 1138 seconds
              (without alignments)
              6318.802 Million cell updates/sec
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Perfect score: 444
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

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Searched:      16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132
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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2:  em_esta: *
3:  em_estum: *
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6:  em_esto: *
7:  em_estpl: *
8:  em_estro: *
9:  em_hic: *
10:  gb_estl: *
11:  gb_est2: *
12:  gb_hic: *
13:  gb_est3: *
14:  gb_est4: *
15:  gb_est5: *
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17:  gb_est: *
18:  em_gss: *
19:  em_gss_hum: *
20:  em_gss_inv: *
21:  em_gss_pln: *
22:  em_gss_vrt: *
23:  em_gss_fun: *
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26:  em_gss_pro: *
27:  em_gss_rod: *

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES						
Result No.	Score	Query Match	Length	DB	ID	Description
1	444	100.0	453	13	BG937925	BG937925 IAB009H06
2	444	100.0	462	13	BG938107	BG938107 IAB011ID05
3	444	100.0	463	13	BG938377	BG938377 IAB016E05
4	444	100.0	464	13	BG938413	BG938413 IAB007G11
5	444	100.0	469	13	BG938112	BG938112 IAB011D11
6	444	100.0	476	13	BG937589	BG937589 IAB003C3

7	444	100.0	476	13	BG938203
8	444	100.0	478	13	BG937601
9	444	100.0	481	13	BG937832
10	444	100.0	482	13	BG937936
11	444	100.0	484	13	BG937881
12	444	100.0	485	13	BG938200
13	444	100.0	486	13	BG937882
14	444	100.0	487	13	BG938101
15	444	100.0	488	13	BG938250
16	444	100.0	491	13	BG937866
17	444	100.0	493	13	BG937861
18	444	100.0	494	13	BG938345
19	444	100.0	497	13	BG937747
20	444	100.0	497	13	BG938042
21	444	100.0	498	13	BG937670
22	444	100.0	502	13	BG937865
23	444	100.0	503	13	BG937991
24	444	100.0	513	13	BG938316
25	444	100.0	525	10	AM654651
26	443	99.8	485	13	BG938044
27	443	99.8	488	13	BG937749
28	442.4	99.6	461	13	BG937779
29	439	98.9	448	13	BG938303
30	439	98.9	484	13	BG938144
31	438	98.6	453	13	BG9378205
32	437	98.4	453	13	BG938205
33	436.4	98.3	456	13	BG937506
34	433.4	97.6	454	13	BG938097
35	433.4	97.6	460	13	BG937777
36	433	97.5	460	13	BG937768
37	433	97.5	462	13	BG938068
38	433	97.5	498	13	BG937733
39	433	97.5	503	13	BG937795
40	432	97.3	448	13	BG937811
41	432	97.3	470	13	BG938187
42	432	97.3	450	13	BG938401
43	432	97.3	487	13	BG938403
44	431.4	97.2	463	13	BG937730
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RESULT 1
BG937925

LOCUS
DEFINITION
B6937925 453 bp mRNA linear EST 11-JUN-2001
1AB009H04 Bovine Abomasum cDNA Library Bos taurus cDNA 5', mRNA
sequence.
B6937925

ACCESSION
VERSION
B6937925.1 GI:14337297
EST.

KEYWORDS
SOURCE
CCW.

ORGANISM
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 453)
Moore,S.S., Hansen,C., Li,C., Fu,A., Meng,Y. and Li,G.
cDNA 5' from bovine abomasum tissue
unpublished (2001)
Contact: Dr. Stephen Moore
Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 AgriFor, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
Tel: 780 492 0169
Fax: 780 492 4265
Email: smoores@afns.ualberta.ca

The sequence best matches gb:BOVLZYM7A (Bos taurus lysozyme 7A mRNA) in main database at high score of 898.0 and E-value of 0.0
PCR primers
FORWARD: M13 Forward
BACKWARD: M13 Reverse

KEYWORDS	SOURCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.	Bos taurus
Moore,S.S., Hansen,C., Li,C., Fu,A., Meng,Y. and Li,G. cDNA's from bovine abomasum tissue Unpublished (2001)	
Contact: Dr. Stephen Moore . Beef Genomics Laboratory Dept of AFNS, University of Alberta 410 Agr./For. Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada Tel.: 780 492 0169 Fax: 780 492 4265 Email: smoores@afns.ualberta.ca The sequence best matches gb:BovLZYM7A (Bos taurus lysozyme 7A mRNA) in main database at high score of 918.0 and E-value of 0.0	
PCR primers FORWARD: M13 Forward BACKWARD: M13 Reverse Seq primer: T3 primer High quality sequence stop: 463 POLYA-No.	
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/sex="Two males and one female mixed"	
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/cell_type="Epithelial"	
/dev_stage="Young adult"	
/lab_host="XLI-BluemRF"-strain"	
/note="Organ: Abomasum; Vector: Uni-ZAPXR; Site_1: EcoR I; Site_2: Xho I"	
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Best Local Similarity	100.0%; Pred. No. 4,9e-125;
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OY 1 ATGAAGGCCTCGTTATTCGTGGGGTTCCTCCTTCCTTCGTGCGTGCCAAAGGCTC 60	
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OY 61 TTGAGAGATGTGACGCTTGCCAGAAGCTGGAAGAACTTGGACGTGACGCTATAAGGGA 120	
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OY 121 GTCAAGCCGGAAGACTGCTGTGTTGCCAAAATGGGAAGCAGTTATACACAAGAACT 180	
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OY -301 GAATTAATGAAAAATGACATGGCTTAACCTGTAGCGGTGGCAAGCATATTGTGCTGAG 360	
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VERSION	BG938413.1	GI:14337785	
KEYWORDS	EST.		
SOURCE	cow.		
ORGANISM	Bos taurus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.		
AUTHORS	1 (bases 1 to 464)		
TITLE	Moore,S.S., Hansen,C., Li,C., Fu,A., Meng,Y. and Li,G.		
JOURNAL	cDNA's from bovine abomasum tissue		
COMMENT	Unpublished (2001)		
	Contact: Dr. Stephen Moore		
	. Beef Genomics Laboratory		
	Dept of AFNS, University of Alberta		
	410 Agri/For. Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada		
	Tel: 780 492 0169		
	Fax: 780 492 4265		
	Email: smoores@atns.ualberta.ca		
	The sequence best matches gb:BOVL2YM7A (Bos taurus lyszyme 7A mRNA		
) in main database at high score of 920.0 and E-value of 0.0		
	PCR primers		
	FORWARD: M13 Forward		
	BACKWARD: M13 Reverse		
	Seq primer: T3 primer		
	POLYA-No.		
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	/dev_stage="Young adult"		
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3			
4	ATGAAGGCTCTGCGTATTCTGGGGTTCTCTCTCTTCTGTCGCTGTCCAGGCAAGTTC	73	
5			
6	TTTGAGAGATGTGAGCTGCCAGAACTCTGAAAGAACTTGACACTGACGCTATAAGGA	120	
7			
8			
9	TTTGAGAGATGTGAGCTGCCAGAACTCTGAAAGAACTTGACACTGACGCTATAAGGA	133	
10			
11			
12	GTCAGCCCTGGGAAACTGGTGTGTTGTTGACCAAAATGGGAAGCAGTTATTAACCAAAAGCT	180	
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14	GTCAGCCCTGGGAAACTGGTGTGTTGTTGACCAAAATGGGAAGCAGTTATTAACCAAAAGCT	193	
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16			
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22			
23	TGGGGTGTATGATGGCAAAACCCCTATGACGCTGTCATGTATCCGACAGC	300	
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25			
26	TGGGGTGTATGATGGCAAAACCCCTATGACGCTGTCATGTATCCGACAGC	313	

QY 301 GAATTAATGAAATGACATCGCTAAAGCTGTACGCTGGCAAGCATATTGTCAGT 360
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 DB 314 GAATTAATGAAATGACATCGCTAAAGCTGTACGCTGGCAAGCATATTGTCAGT 373
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RESULT 5
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 LOCUS 1AB011D12 Bovine Abomasum cDNA Library Bos taurus cDNA 5', mRNA
 DEFINITION
 ACCESSION BG938112
 VERSION BG938112
 KEYWORDS EST.
 SOURCE
 ORGANISM
 Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 Bovidae; Bovinae; Bos.
 1 (bases 1 to 469)
 Moore, S.S., Hansen, C., Li, C., Fu, A., Meng, Y. and Li, G.
 CDNA's from bovine abomasum tissue
 Unpublished (2001)
 CONTACT: Dr. Stephen Moore
 . Beef Genomics Laboratory
 Dept of AFNS, University of Alberta
 410 Agri/For. Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
 Tel: 780 492 0169
 Fax: 780 492 4265
 Email: smoores@afns.ualberta.ca
 The sequence best matches gb:BOVLZYMW7A (Bos taurus lysozyme 7A mRNA
) in main database at high score of 930.0 and E-value of 0.0
 PCR primers
 FORWARD: M13 Forward
 BACKWARD: M13 Reverse
 Seq primer: T3 primer
 High quality sequence stop: 469
 POLYA-No.

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 /cell_type="Epithelial"
 /dev_stage="Young adult"
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 /note="Organ: Abomasum; Vector: Uni-ZAPXR; Site_1: EcoR
 I; Site_2: Xho I"

BASE COUNT 133 a 92 c 123 g 121 t
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 Query Match 100.0%; Score 444; DB 13; Length 469;
 Best Local Similarity 100.0%; Pred. No. 5e-125;
 Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGGCTCTCTATTCCTGGGCTTCTCTCTGCTGCTGCCAAGCAAGTTC 60
 |||||||
 DB 17 ATGAGGCTCTCTATTCCTGGGCTTCTCTCTGCTGCTGCCAAGCAAGTTC 76
 |||||||
 QY 61 TTGAGAGATGTGAGCTGGCAAGCACTGGAAGAACTGAGCTGAGCGCATTAAGGA 120
 |||||||
 DB 77 TTGAGAGATGTGAGCTGGCAAGCACTGGAAGAACTGAGCTGAGCGCATTAAGGA 136
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QY 121 GTCAGCTGGCAAGCTGTTGTGTTGACCAATGGGAAGACGTTATACCAAAAGCT 180
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 DB 137 GTCAGCTGGCAAGCTGTTGTGTTGACCAATGGGAAGACGTTATACCAAAAGCT 196
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 QY 181 ACAAACTACAACTCTAGCAGTGAAGCACTGATTAATGGATATTTTCAGATCAACAGCAA 240
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 DB 197 ACAAACTACAACTCTAGCAGTGAAGCACTGATTAATGGATATTTTCAGATCAACAGCAA 256
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 QY 241 TGGTGTGTTAATGATGCGCAAAACCCCTAATGCAATTGACGCTGTCATGTCGACG 300
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 DB 257 TGGTGTGTTAATGATGCGCAAAACCCCTAATGCAATTGACGCTGTCATGTCGACG 316
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 QY 301 GAATTAATGAAATGACATCGCTAAAGCTGTACGCTGGCAAGCATATTGTCAGT 360
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 DB 317 GAATTAATGAAATGACATCGCTAAAGCTGTACGCTGGCAAGCATATTGTCAGT 376
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 QY 361 CAAGCATTTACAGCTGGTGGCATGGAAGATGATGTCGAGACCATGAGTGCAGAGT 420
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 DB 377 CAAGCATTTACAGCTGGTGGCATGGAAGATGATGTCGAGACCATGAGTGCAGAGT 436
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 QY 421 TACGTTGAGGCTTGCACCTGTAA 444
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 DB 437 TACGTTGAGGCTTGCACCTGTAA 460
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RESULT 6
 BG937589 476 bp mRNA linear EST 11-JUN-2001
 LOCUS 1AB003C3 Bovine Abomasum cDNA Library Bos taurus cDNA 5', mRNA
 DEFINITION
 ACCESSION BG937589
 VERSION BG937589
 KEYWORDS EST.
 SOURCE
 ORGANISM
 Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 Bovidae; Bovinae; Bos.
 1 (bases 1 to 476)
 Moore, S.S., Hansen, C., Li, C., Fu, A., Meng, Y. and Li, G.
 CDNA's from bovine abomasum tissue
 Unpublished (2001)
 CONTACT: Dr. Stephen Moore
 . Beef Genomics Laboratory
 Dept of AFNS, University of Alberta
 410 Agri/For. Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
 Tel: 780 492 0169
 Fax: 780 492 4265
 Email: smoores@afns.ualberta.ca
 The sequence best matches gb:BOVLZYMW7A (Bos taurus lysozyme 7A mRNA
) in main database at high score of 944.0 and E-value of 0.0
 PCR primers
 FORWARD: M13 Forward
 BACKWARD: M13 Reverse
 Seq primer: T3 primer
 High quality sequence stop: 476
 POLYA-No.

FEATURES
 source location/Qualifiers

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 /sex="Two males and one female mixed"
 /tissue_type="Gastrointestinal tissue (GIT)"
 /cell_type="Epithelial"
 /dev_stage="Young adult"
 /lab_host="X11-BlueRF"-strain"
 /note="Organ: Abomasum; Vector: Uni-ZAPXR; Site_1: EcoR
 I; Site_2: Xho I"

BASE COUNT 135 a 94 c 122 g 125 t
 ORIGIN
 Query Match 100.0%; Score 444; DB 13; Length 476;

QY 241 TGGTGTATGATGAGCAAAACCCCTAATGAGCGCTGCATGATCTGCAGC 300
 DB 254 TGGTGTATGATGAGCAAAACCCCTAATGAGCGCTGCATGATCTGCAGC 313
 QY 301 GAATTAATGAAAATGACATCGCTAAAGCTGAGCGTGCAAGCATATTTGCTAGTGA 360
 DB 314 GAATTAATGAAAATGACATCGCTAAAGCTGAGCGTGCAAGCATATTTGCTAGTGA 373
 QY 361 CAAGGCATTACGCTGGGTGGCATGGAAGATCATTTGCGAGACATGACCTCAGCACT 420
 DB 374 CAAGGCATTACGCTGGGTGGCATGGAAGATCATTTGCGAGACATGACCTCAGCACT 433
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 DB 434 TACGTTGAGGGTTGCACCCCTGTAA 457

RESULT 12
 BG938200 485 bp mRNA linear EST 11-JUN-2001
 LOCUS 1AB013G04 Bovine Abomasum cDNA Library Bos taurus cDNA 5', mRNA
 DEFINITION
 ACCESSION BG938200
 VERSION BG938200.1 GI:14337572
 KEYWORDS EST.
 SOURCE
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.
 1 (bases 1 to 485)
 Moore,S.S., Hansen,C., Li,C., Fu,A., Meng,Y. and Li,G.
 cDNA's from bovine abomasum tissue
 Unpublished (2001)
 COMMENT
 CONTACT: Dr. Stephen Moore
 Beef Genomics Laboratory
 Dept of AFNS, University of Alberta
 410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
 Tel: 780 492 0169
 Fax: 780 492 4265
 Email: smoores@afns.ualberta.ca
 The sequence best matches gb:BOVL2YM7A (Bos taurus lysozyme 7A mRNA
) in main database at high score of 961.0 and E-value of 0.0
 PCR PRIMERS
 FORWARD: M13 Forward
 BACKWARD: M13 Reverse
 Seq primer: T3 primer
 High quality sequence stop: 485
 POLYA-NO.

FEATURES
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 location/Qualifiers
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 /organism="Bos taurus"
 /db_xref="taxon:9913"
 /clone_id="Bovine Abomasum cDNA Library"
 /sex="Two males and one female mixed"
 /tissue_type="Gastrointestinal tissue (GIT)"
 /cell_type="Epithelial"
 /dev_stage="Young adult"
 /lab_host="XLI-BlueMRF-strain"
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 I; Site_2: Xho I"

BASE COUNT 137 a 97 c 123 g 128 t

ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 5e-125;
 Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAGGCTCTGCTATTCCTGAGGGTTCCTCTCTCTGCTGCTGCCAAGCAAGGTC 60
 DB 15 ATGAAGGCTCTGCTATTCCTGAGGGTTCCTCTCTCTGCTGCTGCCAAGCAAGGTC 74

QY 61 TTGAGAGATGTGAGCTTGCCAGACTCTGAAGAACTTGAGCTGAGCGGTATAGGGA 120
 DB 75 TTGAGAGATGTGAGCTTGCCAGACTCTGAAGAACTTGAGCTGAGCGGTATAGGGA 134
 QY 121 GTACCCCTGGCAAACTGGTTGTGTTGAACCAATGGAAAGCAGTTATTAACAAAAGCT 180
 DB 135 GTACCCCTGGCAAACTGGTTGTGTTGAACCAATGGAAAGCAGTTATTAACAAAAGCT 194
 QY 181 ACAAACTCAATCCCTAGCAGTGAAGACATGTTATGGGATATTTCAATCAACAGCAA 240
 DB 195 ACAAACTCAATCCCTAGCAGTGAAGACATGTTATGGGATATTTCAATCAACAGCAA 254
 QY 241 TGGTGTATGATGAGCAAAACCCCTAATGAGCGCTGCATGATCTGCAGC 300
 DB 255 TGGTGTATGATGAGCAAAACCCCTAATGAGCGCTGCATGATCTGCAGC 314
 QY 301 GAATTAATGAAAATGACATCGCTAAAGCTGAGCGTGCAAGCATATTTGCTAGTGA 360
 DB 315 GAATTAATGAAAATGACATCGCTAAAGCTGAGCGTGCAAGCATATTTGCTAGTGA 374
 QY 361 CAAGGCATTACGCTGGGTGGCATGGAAGATCATTTGCGAGACATGACCTCAGCACT 420
 DB 375 CAAGGCATTACGCTGGGTGGCATGGAAGATCATTTGCGAGACATGACCTCAGCACT 434
 QY 421 TACGTTGAGGGTTGCACCCCTGTAA 444
 DB 435 TACGTTGAGGGTTGCACCCCTGTAA 458

RESULT 13
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 LOCUS 1AB009C07 Bovine Abomasum cDNA Library Bos taurus cDNA 5', mRNA
 DEFINITION
 ACCESSION BG937882
 VERSION BG937882.1 GI:14337254
 KEYWORDS EST.
 SOURCE
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.
 1 (bases 1 to 486)
 Moore,S.S., Hansen,C., Li,C., Fu,A., Meng,Y. and Li,G.
 cDNA's from bovine abomasum tissue
 Unpublished (2001)
 COMMENT
 CONTACT: Dr. Stephen Moore
 Beef Genomics Laboratory
 Dept of AFNS, University of Alberta
 410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
 Tel: 780 492 0169
 Fax: 780 492 4265
 Email: smoores@afns.ualberta.ca
 The sequence best matches gb:BOVL2YM7A (Bos taurus lysozyme 7A mRNA
) in main database at high score of 963.0 and E-value of 0.0
 PCR PRIMERS
 FORWARD: M13 Forward
 BACKWARD: M13 Reverse
 Seq primer: T3 primer
 High quality sequence stop: 486
 POLYA-NO.

FEATURES
 source
 location/Qualifiers
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 /organism="Bos taurus"
 /db_xref="taxon:9913"
 /clone_id="Bovine Abomasum cDNA Library"
 /sex="Two males and one female mixed"
 /tissue_type="Gastrointestinal tissue (GIT)"
 /cell_type="Epithelial"
 /dev_stage="Young adult"
 /lab_host="XLI-BlueMRF-strain"
 /note="Organ: Abomasum; Vector: Uni-22APXR; Site_1: Ecor
 I; Site_2: Xho I"

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OM nucleic - nucleic search, using sw model

Run on: July 5, 2003, 05:28:27 ; Search time 42 Seconds
(without alignments)
3242.011 Million cell updates/sec

Title: US-09-978-199-1

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Sequence: 1 atgaagctccgtattct.....ttgggggttgaccctgttaa 444

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Issued Patents, NA:

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	439	98.9	964	1	US-07-798-223A-1
2	250	56.3	657	4	US-09-385-982-344
3	157.2	35.4	394	6	5182195-1
4	153	34.5	396	1	US-08-503-584-6
5	122.2	27.5	586	1	US-08-385-590A-3
6	122.2	27.5	586	3	US-09-021-520-3
7	63.8	14.4	222	4	US-09-388-917-1
8	63	14.2	610	4	US-09-786-023-3
9	48.4	10.9	301	4	US-09-388-917-2
10	43	9.7	7218	1	US-08-332-463-14
11	41.2	9.3	396	1	US-08-385-590A-1
12	41.2	9.3	396	3	US-09-021-520-1
13	32.2	7.3	4374	2	US-08-449-644-3
14	32.2	7.3	4374	2	US-08-449-644-3
15	32	7.2	2082	4	US-09-440-325A-2
16	31.6	7.1	1676	4	US-08-336-165A-212
17	31.4	7.1	1499	3	US-08-889-841B-24
18	31.4	7.1	1499	3	US-08-889-841B-27
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23	31.4	7.1	3726	1	US-08-605-672-1
24	31.4	7.1	3726	2	US-08-482-293A-1
25	31.4	7.1	3726	2	US-08-943-363-1
26	31.4	7.1	3726	4	US-09-193-043-1
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29	31.4	7.1	3785	1	US-08-605-672-98	Sequence 98, Appl
30	31.4	7.1	3785	2	US-08-482-293A-98	Sequence 98, Appl
31	31.4	7.1	3785	2	US-08-943-363-98	Sequence 98, Appl
32	31.4	7.1	3785	4	US-09-193-043-98	Sequence 98, Appl
33	31.4	7.1	3785	4	US-09-688-307A-98	Sequence 98, Appl
34	31.4	7.1	3956	1	US-08-485-618-97	Sequence 97, Appl
35	31.4	7.1	3956	1	US-08-605-672-97	Sequence 97, Appl
36	31.4	7.1	3956	2	US-08-482-293A-97	Sequence 97, Appl
37	31.4	7.1	3956	2	US-08-943-363-97	Sequence 97, Appl
38	31.4	7.1	3956	4	US-09-193-043-97	Sequence 97, Appl
39	31.4	7.1	3956	4	US-09-688-307A-97	Sequence 97, Appl
40	31	7.0	4371	4	US-09-462-136-8	Sequence 8, Appl
41	31	7.0	11459	4	US-09-462-136-7	Sequence 7, Appl
42	30	6.8	1035	4	US-09-457-066-6	Sequence 6, Appl
43	30	6.8	1773	4	US-02-134-001C-1553	Sequence 1553, Ap
44	29.8	6.7	1408	3	US-08-889-841B-22	Sequence 22, Appl
45	29.8	6.7	1497	2	US-07-916-098A-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-07-798-223A-1
Sequence 1, Application US/07798223A
Patent No. 5422108
GENERAL INFORMATION:
APPLICANT: Mirkov, T. Erik
APPLICANT: Fitzmaurice, Leona Claire
TITLE OF INVENTION: Protection of Plants Against Pathogens
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitch, Even, Tabin & Flannery
STREET: 135 South LaSalle Street, Suite 900
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07798, 223A
FILING DATE: 19911125
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/762, 679
FILING DATE: 19-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 51984
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)552-1311
TELEFAX: (619)552-0095
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 964 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 25..459
US-07-798-223A-1
Query Match 98.9%; Score 439; DB 1; Length 964;
Best Local Similarity 100.0%; Pred. No. 1.5e-133;
Matches 439; Conservative 0; Indels 0; Gaps 0;

OY	6	GGCGTCGTAATTCGTGGGGTTTCTTCCTTCTGTGCGGTGCCAAGGCAAGTCTTTGA	65
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OY	66	GAGATGTGACCTTGGCCAGAACTCTGAAGAACTTGAGTGAACGCGCTTTAAGGGAGTCAG	125
Db	84	GAGATGTGACCTTGGCCAGAACTCTGAAGAACTTGAGTGAACGCGCTTTAAGGGAGTCAG	143
OY	126	CGTGGCAAACTGGTCTGTGTTGACCAAAATGGGAAAGCAGTTTAAACAAAAAGCTACAAA	185
Db	144	CGTGGCAAACTGGTCTGTGTTGACCAAAATGGGAAAGCAGTTTAAACAAAAAGCTACAAA	203
OY	186	CTACAACTCCAGAGAGGAAAGCAGTGTATTGGATTATTCAGATCAACAGCAAAATGGTG	245
Db	204	CTACAACTCCAGAGAGGAAAGCAGTGTATTGGATTATTCAGATCAACAGCAAAATGGTG	263
OY	246	GTGTAATGATGCGCAAAACCCCTTAATGACAGTTGACGGCTGTCAATGATCTTGACAGCAATT	305
Db	264	GTGTAATGATGCGCAAAACCCCTTAATGACAGTTGACGGCTGTCAATGATCTTGACAGCAATT	323
OY	306	AATGSAAAATGACATGCTAAAGCTGTACGTTGCTCAAGACATATTGTCAGTGGAGCAAG	365
Db	324	AATGSAAAATGACATGCTAAAGCTGTACGTTGCTCAAGACATATTGTCAGTGGAGCAAG	383
OY	366	CATTACAGCCTGGGTGGCGATGGAAAAAGTCATTGTGAGAACCATGACGTCACAGCTTAAGT	425
Db	384	CATTACAGCCTGGGTGGCGATGGAAAAAGTCATTGTGAGAACCATGACGTCACAGCTTAAGT	443
OY	426	TGAGGGTTGCAACCCCTGTA 444	
Db	444	TGAGGGTTGCAACCCCTGTA 462	

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RESULT 2
US-09-385-982-344
; Sequence 344, Application US/09385982
; Patent No. 6262334
; GENERAL INFORMATION:
; APPLICANT: ENDEGE, WILSON O., ET AL.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; TITLE OF INVENTION: PRODUCTS: 11
; FILE REFERENCE: CCDNA-260xx
; CURRENT APPLICATION NUMBER: US/09/385,982
; CURRENT FILING DATE: 1999-08-30
; EARLIER APPLICATION NUMBER: 09/328,111
; EARLIER FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: 60/117,393
; EARLIER FILING DATE: 1999-01-27
; EARLIER APPLICATION NUMBER: 60/098,639
; EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 544
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 344
; LENGTH: 657
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(657)
; OTHER INFORMATION: n = A,T,C or G
; US-09-385-982-344

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				Gaps 1
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Db	15	TGTGTTGGGGCTTGCTCTCTCTTTGTACGGTCCAGGGCAAGCTTTGAAGAAGTGS	74	
QY	74	ACCTTGCCGAACTCTGAAGAACTTGGACATGGAACGGCTATAGGGAGTACCTTGCCA	133	

Db	75	AGTTGGCCAAACAATCTGAAAAGATTGGGAATGGATGGCTACAGGGGAATCAGCTACGAA	134
QY	134	ACGTGTTGTGTTTGGACCAATATGGGAAGACGTTATTAACAACAAACCTACAACTACATC	193
Db	135	ACGGATGTTTGTGGCCCAATGGGGAAGGTTTACACACAGGCTACAAACCTACATATG	194
QY	194	CTAGCAGTGAACCACTGATTTATGGGATTTTACATCAACAGCAAAATGGGGGTATG	253
Db	195	CTGGAGACGACAGCACTGATTTATGGGATTTTCAATCAATTAAGCCGCTACTGCTGTATG	254
QY	254	ATGGCAAAACCCCTAATGCAAGTTGAAGGCTGCATGATCTCGACAGCAATTAATGAAA	313
Db	255	ATGGCAAAACCCGAGGACGATTAATGCGTGCATTTCTGGCAGTCTTGGTGCAG	314
QY	314	ATGACATCGCTAAAGCTGTAGCGTGTGCCAAGCATATTGTC-----AGTAGCAAGGCAT	368
Db	315	ATACATCGCTGATGCTGTAGCTTGTGCAAAAANAGTTGTCCTCCGATGCCAAGGCATT	374
QY	369	TACAGCGTGGGTGGCATGGAAGAAGCATTTGTGCAAGACCATAGCTCAGCACTTACGTTGA	428
Db	375	AAGAGCATGGGTGGCATGGAAGAATCGTTGTAACAGAGATGTCGCACTATGTTCAA	434
QY	429	GGGT	432
Db	435	NGGT	438

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RESULT 3
5182195-1
; Patent No. 5182195
; APPLICANT: NAKAHAMA, KAZUO; KAISHO, YOSHIHIKO; YOSHIMURA, KOJI
; TITLE OF INVENTION: METHOD FOR INCREASING USING PROTEASE
; DEFICIENT YEASTS
; NUMBER OF SEQUENCES: 71
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/269,140
; FILING DATE: 09-NOV-1988
; SEQ ID NO:1:
; LENGTH: 394
5182195-1

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Query Match	35.4%	Score 157.2	DB 6	Length 394
Best Local Similarity	64.8%	Pred. No. 7.3e-42		
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QY	122	TCAGCCTGGCAAACTGTGTGTTTGACCAAATGGGAAAGACGTTATTAACAAAAAGCTA	181	
Db	61	TTTTCTTTACCCACACGTGATGTCTTGCTGAATGTTGGAAATCCGGCTATTAACATAGAGCTA	120	
QY	182	CAAACCTACAMTCTTAGACAGTGAAGCAAGCATGTATTAAGGATATTTACAGATCAACAGCAAAAT	241	
Db	121	CCAAATTACAAAGCTGGCGACGGTCTCTACAGACTATGTGATTTTCCAAATTAACCTCAGAT	180	
QY	242	GGTGGTGTATATGATGGCAAAACCCCTAATGACGTTGAAGCGCTCATGATTCCTGACGGC	301	
Db	181	ATTGGTGTAAACATGGCAAGACTCCAGGTGCCCTCAACGCCCTCATCTTCTTGCTCAG	240	
QY	302	AATTAATGAAATACATGCTCTAAAGGTGTAGGCTGTGCAAAAGCATATTGTACAGCA--	359	
Db	241	CTTTGCTTCAGGACAACTTCTGTATGTGTGTGCTCTCGCTAAGAGAGTTGTCCTCGGACCC	300	
QY	360	-GCAAGGCAATTACAGCCCTGAGTGCATAGCAAAATCTAATTCAGAGACCATAGACGTGACA	418	
Db	301	CACAGGGATTAAGACCTCGGGTCGCTTGGAGAAACAGATGCCAAAAATTAAGAGATGTACAGC	360	
QY	419	GTTACGTTGAGGTTGCACCTGTAA 444		
Db	361	AATACGTTCAAGGTTGTGTGTTTAA 386		

Best Local Similarity 57.7%; Pred. No. 2.3e-30; Matches 258; Conservative 0; Mismatches 183; Indels 6; Gaps 2

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QY      1 ATGAAGCTCTCGTTATTCCTGGGGTTTCTCTCTTTCTGTCGCTCCAAAGCAAGTC 60
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Db      90 TTTGAGCATGTGACCTGGCAGCGGCTATGAAGCCTCAAGACTTGATTAATCTGGGGA 149
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Db      150 TACACCTCGGGAAACTGGGTGTGTTCACAAATTCGAGAGTAACTTCAACCCACGAGCT 209
QY      181 ACAAACTCAATTCCTACAGCAGTGAAGACACTGATTTGGGATATTCACATCAACAGCAAA 240
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QY      301 GAATTAATGAAAAATGACATGCTTAAAGCTTAGAGGTGTGCAAAAGCATATTTGTGAG--T 357
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OY	358	GAGCAAGGCATTACAGCCTGGGTGGCATGAAAAATCATTTGCGAGACATGACGTCAGC	417
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OY	418	AGTACGCTGAGGGTTGGACCCTCTAA	444
Dd	447	GCGTGATCAGAGGCTGCCGGCTGTGA	473

Sequence 1, Application US/09388917
Patent No. 6258542
GENERAL INFORMATION:
APPLICANT: Hayashizaki, Yoshihide
TITLE OF INVENTION: Method for Supporting DNA-Fixation and DNA-Fixed
TITLE OF INVENTION: Support
FILE REFERENCE: 1794-0120P
CURRENT APPLICATION NUMBER: US/09/388, 917
CURRENT FILING DATE: 1999-09-02
EARLIER APPLICATION NUMBER: 10-250619
EARLIER FILING DATE: 1998-09-04
EARLIER APPLICATION NUMBER: 11-240910
EARLIER FILING DATE: 1999-08-27

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: NUMBER OF SEQ. ID NOS: 7
: SOFTWARE: PatentIn Ver. 2.0
: SEQ. ID NO. 1
: LENGTH: 222
: TYPE: DNA
: ORGANISM: Gallus gallus
US-09-388-917-1

Query Match      14.4%;      Score 63.8;  DB 4;      Length 222;
Best Local Similarity 63.2%;
Pred. No. 1.6e-11;
Matches 98; Conservative 0; Mismatches 57; Indels 0; gaps 0;

QY      1  ATCAAGCGCTCTCTATTTCGGGGTTCCTTCCTTCCTTCGTCGCTTCGCAAGCGCAGGTC 60

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[illegible]


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: CURRENT APPLICATION DATA:

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MEDIUM TYPE: Floppy disk

Result No.	Score	Query Match	Length	DB	ID	Description
1	444	100.0	444	10	US-09-978-189-1	Sequence 1, Appl
2	444	100.0	10132	10	US-09-978-189-3	Sequence 3, Appl
3	279	62.8	748	10	US-09-969-347-118	Sequence 318, App
4	267.8	60.3	478	9	US-10-046-935-1085	Sequence 1085, App
5	267.8	60.3	478	9	US-09-878-178-1085	Sequence 1085, App
6	267.8	60.3	478	9	US-10-146-502-1085	Sequence 1085, App
7	265.2	59.7	2467	9	US-10-001-873-11	Sequence 11, Appl
8	250	52.8	657	9	US-09-871-161-334	Sequence 344, App
9	190	46.3	606	9	US-10-060-036-2344	Sequence 2344, App
10	185.4	41.8	582	9	US-10-046-935-1606	Sequence 1606, App
11	185.4	41.8	582	9	US-09-878-178-1606	Sequence 1606, App
12	185.4	41.8	582	9	US-10-146-502-1606	Sequence 1606, App
13	172.6	38.9	367	9	US-09-746-692-8055	Sequence 8055, App
14	172.6	38.9	367	9	US-10-040-862-8055	Sequence 8055, App
15	172.6	38.9	52	9	US-10-102-524-791	Sequence 791, App
16	172.6	38.9	636	9	US-09-796-692-8226	Sequence 8226, App
17	172.6	38.9	636	9	US-10-040-862-8226	Sequence 8226, App
18	163.6	36.8	233	9	US-10-114-666-117	Sequence 117, App
19	163.6	36.8	233	10	US-09-895-828-117	Sequence 117, App

20	151.4	34.1	393	9	US-10-076-816-1	Sequence 1, App
21	151.4	34.1	393	9	US-10-077-384-1	Sequence 1, App
22	140	31.5	446	9	US-10-066-543-3129	Sequence 3129, Ap
23	109.6	24.7	479	9	US-10-025-380-526	Sequence 526, App
24	109.6	24.7	479	10	US-09-922-217-526	Sequence 526, App
25	109.6	24.7	479	10	US-09-893-263-526	Sequence 526, Ap
26	83.6	18.8	575	9	US-09-796-692-8818	Sequence 8818, Ap
27	83.6	18.8	575	9	US-10-040-862-8818	Sequence 8818, Ap
28	80.2	18.1	950	9	US-09-978-295A-220	Sequence 220, App
29	80.2	18.1	950	9	US-09-978-697-220	Sequence 220, App
30	80.2	18.1	950	9	US-09-978-192A-220	Sequence 220, App
31	80.2	18.1	950	9	US-09-999-832A-220	Sequence 220, App
32	80.2	18.1	950	9	US-09-978-189-220	Sequence 220, App
33	80.2	18.1	950	9	US-10-028-072-407	Sequence 407, App
34	80.2	18.1	950	9	US-10-121-049-407	Sequence 407, App
35	80.2	18.1	950	9	US-10-123-904-407	Sequence 407, App
36	80.2	18.1	950	9	US-10-140-470-407	Sequence 407, App
37	80.2	18.1	950	9	US-10-175-746-407	Sequence 407, App
38	80.2	18.1	950	9	US-10-176-921-407	Sequence 407, App
39	80.2	18.1	950	9	US-10-176-921-407	Sequence 407, App
40	80.2	18.1	950	9	US-10-137-865-407	Sequence 407, App
41	80.2	18.1	950	9	US-10-140-474-407	Sequence 407, App
42	80.2	18.1	950	9	US-10-142-431-407	Sequence 407, App
43	80.2	18.1	950	9	US-10-143-114-407	Sequence 407, App
44	80.2	18.1	950	9	US-10-140-002-407	Sequence 407, App
45	80.2	18.1	950	9	US-09-978-608A-220	Sequence 220, App

ALIGNMENTS

```

RESULT 1
US-09-978-199-1
: Sequence 1, Application US/09978199
: Patent No. US20020104126A1
: GENERAL INFORMATION:
: APPLICANT: POCUE, GREGORY P.
: APPLICANT: VELICHKO, SHARLENE
: TITLE OF INVENTION: PRODUCTION OF BOVINE LYSSOZYME BY PLANT VIRAL VECTORS
: FILE REFERENCE: 42202
: CURRENT APPLICATION NUMBER: US/09/978,199
: CURRENT FILING DATE: 2001-10-17
: PRIOR APPLICATION NUMBER: 60/240,967
: PRIOR FILING DATE: 2000-10-18
: NUMBER OF SEQ ID NOS: 3
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 1
: LENGTH: 444
: TYPE: DNA
: ORGANISM: Bovine sp.
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(441)
US-09-978-199-1

```

Query Match	100.0%;	Score 444;	DB 10;	Length 444;
Best Local Similarity	100.0%;	Pred. No. 7	le-134;	
Matches 444;	Conservative	0;	Mismatches 0;	Indels 0;
			Gaps	0;
QY	1	ATAGAAGCTCTGTTATTCCTGGGCTTCTCTCTCTGCTGCGCCAAAGGCAAGTGC	60	
Db	1	ATAGAAGCTCTGTTATTCCTGGGCTTCTCTCTCTGCTGCGCCAAAGGCAAGTGC	60	
QY	61	TTTGGAGATGTGACGCTTGCAGAACTCTGGAAGAACTTGAGCTGACGCGCTTAAGGCA	120	
Db	61	TTTGGAGATGTGACGCTTGCAGAACTCTGGAAGAACTTGAGCTGACGCGCTTAAGGCA	120	
QY	121	GTCAGCGCTGGCAAACTGCTGTTGTTTGACAAATGGGAAAGCAGTTATTAACAACAAAGCT	180	
Db	121	GTCAGCGCTGGCAAACTGCTGTTGTTTGACAAATGGGAAAGCAGTTATTAACAACAAAGCT	180	
QY	181	ACAAACTAACAATCCAGCAGTGAAGCAACGATATATGAGATTTTCAGATCAACACAA	240	
Db	181	ACAAACTAACAATCCAGCAGTGAAGCAACGATATATGAGATTTTCAGATCAACACAA	240	

Db	181	ACAACTACAAATCCTFAGCAGTGAAGACACTGATTATGGGAAATTTTCAGATCAACAGCAA	240
Qy	241	TGTTGGTGTAAATGATGAGCAAAAACCCCTTAATGCAGTTCAGGCGTCTCATGTATCCGTGAGC	300
Db	241	TGTTGGTGTAAATGATGAGCAAAAACCCCTTAATGCAGTTCAGGCGTCTCATGTATCCGTGAGC	300
Qy	301	GAATTAATGAAAAATGACATCGCTTAAACCTGTAGCGGTGCGAAAGCATATTGTCAAGTGA	360
Db	301	GAATTAATGAAAAATGACATCGCTTAAACCTGTAGCGGTGCGAAAGCATATTGTCAAGTGA	360
Qy	361	CAAGCATTTACACCTTGGGTGGCATGAAAAATCATTTGTGAGACCATGACGTACAGT	420
Db	361	CAAGCATTTACACCTTGGGTGGCATGAAAAATCATTTGTGAGACCATGACGTACAGT	420
Qy	421	TACGTTAGAGGTTGCACCCCTGTAA	444
Db	421	TACGTTAGAGGTTGCACCCCTGTAA	444

```

RESULT 2
US-09-978-199-3
: Sequence 3, Application US/09978199
: Patent No. US20020104126A1
: GENERAL INFORMATION:
: APPLICANT: POCHE, GREGORY P.
: APPLICANT: VELICHKO, SHARLENE
: TITLE OF INVENTION: PRODUCTION OF BOVINE LYSOZYME BY PLANT VIRAL VECTORS
: FILE REFERENCE: 42202
: CURRENT APPLICATION NUMBER: US/09/978,199
: PRIORITY FILING DATE: 2001-10-17
: PRIOR APPLICATION NUMBER: 60/240,967
: PRIORITY FILING DATE: 2000-10-18
: NUMBER OF SEQ ID NOS: 3
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 3
: LENGTH: 10132
: TYPE: DNA
: ORGANISM: Bovine sp.
: US-09-978-199-3

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	Query Match	100.0%; Score 444; DB 10; Length 10132;
	Best Local Similarity	100.0%; Pred. No. 4.1e-133.
	Matches 444; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1	ATGAAGCCTCTCGTATTTCGTGGGTTTCCTCTCCCTTTCTGTGCTGCCAAGSCAAGTC 60
Dd	5767	ATGAAGGCCTCTCGTATTTCGTGGGTTTCCTCTCCCTTTCTGTGCTGCCAAGSCAAGTC 5828
QY	61	TTTGAGAGATGAGACCTTGCAGAACTCTGAAGAACCCTGGACTGGAGCGCTATAAGGGA 120
Dd	5827	TTTGAGAGATGAGACCTTGCAGAACTCTGAAGAACCCTGGACTGGAGCGCTATAAGGGA 5888
QY	121	GTCAGCCTGGCAAACTGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACAACAAAGCT 180
Dd	5887	GTCAGCCTGGCAAACTGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACAACAAAGCT 5948
QY	181	ACAAACTCAATCCAGCAGTGAAGAAGCATTAATGGGATATTACAGATCAACAGCAA 240
Dd	5947	ACAAACTCAATCCAGCAGTGAAGAAGCATTAATGGGATATTACAGATCAACAGCAA 6006
QY	241	TGCTGGTGAATGATGGCAAAACCCCAATGCAAGTTAGAGCGCTGTCATATATCTGCAGC 300
Dd	6007	TGCTGGTGAATGATGGCAAAACCCCAATGCAAGTTAGAGCGCTGTCATATCTGCAGC 6066
QY	301	GAATTAATGGAANAATGACATCGCTTAAGCGTGTAGCTGTGCAAAAGCATATTGTCACTAG 360
Dd	6067	GAATTAATGGAANAATGACATCGCTTAAGCGTGTAGCTGTGCAAAAGCATATTGTCACTAG 6126
QY	361	CAAGCATTAAAGCCTGGGTGGCATGTGAAGAACATTTGTCAGACCATCAGCTGCAGCT 420
Dd	6127	CAAGCATTAAAGCCTGGGTGGCATGTGAAGAACATTTGTCAGACCATCAGCTGCAGCT 6186
QY	421	TACGTTGAGGGTTGCACCTCTGA 444

Db 6187 TACGTGAGGGTTGCACCCTGTAA 6210

RESULT 3
 US-09-969-347-318
 : Sequence 318, Application US/09969347
 : Patent No. US20020115085A1
 : GENERAL INFORMATION:
 : APPLICANT: Ebner, Reinhard
 : TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign
 : TITLE OF INVENTION: Sets
 : FILE REFERENCE: 689290-69
 : CURRENT APPLICATION NUMBER: US/09/969, 347
 : CURRENT FILING DATE: 2001-10-02
 : PRIOR APPLICATION NUMBER: US/60/237, 598
 : PRIOR FILING DATE: 2000-10-03
 : PRIOR APPLICATION NUMBER: US/60/237, 604
 : PRIOR FILING DATE: 2000-10-03
 : NUMBER OF SEQ ID NOS: 318
 : SOFTWARE: Patentin version 3.0
 : SEQ ID NO 318
 : LENGTH: 748
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 : US-09-969-347-318

Query Match	62.8%	Score	279	DB	10	Length	748
Best Local Similarity	78.1%	Pred.	No.	3	5e-80		
Matches	349	Conservative	0	Mismatches	95	Indels	3
							Gaps
							1
QY	1	ATGAGGCTCTCGTTATTTCTGGGGGTTTCTCTTCTCTGTCGTGCTCCAGGCAAGTTC	60				
Db	14	ATGAGGCTCTCGTTATTTCTGGGGGTTTCTCTTCTCTGTTACGGTCCAGGCAAGTTC	73				
QY	61	TTTGAGAGTGTGACCTTGCAGAACTGTGAAGAAATTGAGCTGAGCGGTATAAGGA	120				
Db	74	TTTGAAAGGTGTGACTTGGCCAGAACTCTGAAGAAATTGGAATGGATGGCTTACAGGGA	133				
QY	121	GTGAGCGTGGCAAACTGGTTGTGTTTGAACCAATGGGAAAGAGTATAACAAAAAGCT	180				
Db	134	ATGAGCGTGGCAAACTGGATGTGTTTGGCCAAATGGGAGAGTGTATACAAACAGAGCT	193				
QY	181	ACAAACTCAATCCAGAGTGAAGAAAGACATGATATGGATATTTGATCAACAAAGCAA	240				
Db	194	ACAAACTCAATGCTGGAGACAGAAAGCACTGATATGGATATTTGATCAACAAAGCCG	253				
QY	241	TGGTGGTGTAAATGATGCAAAACCCCTAATGCAAGTTGACGCTGTCATGTATCTGACG	300				
Db	254	TACTGGTGTAAATGATGCAAAACCCCGAGAGCAAGTTAATCTGTCAATTTATCTGACG	313				
QY	301	GAAATTAATGAAAAATGAAATGCAATGCTTAAGCGTGTAGCGTGCACAAAGCATATTGTCACTGA	359				
Db	314	GCTTGTGTCAGAAATGAAATGCAATGCTGTAAGCTGTAGCTGTGTCAAAGAGGGTGTCCGTAT	373				
QY	360	--GCAAGGCATTACAGCTGGTGGTGGCATGGAAGAAAGTCATGTGCAAGCAACCATACCTGAC	417				
Db	374	CCACAAGGCATTAGAGCATGGGTGGCATGGGGAAGATGTTGTCAAAAAGCAAGATGTCCGT	433				
QY	418	AGTTACGTTGAGGGTGTGACCCCTTAA	444				
Db	434	CAGTATGTTCAAGGTTGTGAGACTTAA	460				

RESULT 4
US-10-046-935-1085
Sequence 1085, Application US/10046935
Patent No. US20020156011A1
GENERAL INFORMATION:
APPLICANT: Jiang, Yugu
APPLICANT: Harlocker, Susan L.
APPLICANT: Secrist, Heather
APPLICANT: Wang, Aijun

Db 122 GGATGTGTTGGCCAAATGGGAGAGTGGTTACAAACACAGAGTACAACTACATGCTG 181
QY 197 GCAGTGAAGACACTGATTTATGGGATTTATTCAGATCAACAGCAATGTTGTTATGATG 256
Db 182 GAGCAGAGACGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 241
QY 257 GCAAAACCCCTTAATGACGATGACGATGACGATGACGATGACGATGACGATGACG 316
Db 242 GCAAAACCCCTTAATGACGATGACGATGACGATGACGATGACGATGACGATGACG 301
QY 317 ACATGCGTAAAGCTGTAGCGGTGCAAGATGATGATGATGATGATGATGATGATG 373
Db 302 ACATGCGTAAAGCTGTAGCGGTGCAAGATGATGATGATGATGATGATGATGATG 361
QY 374 CCTGGGTGCGATGGAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 433
Db 362 CATGGGTGCGATGGAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 421
QY 434 GCACCCCTGTAA 444
Db 422 GTGAGTGTAA 432

RESULT 7

US-10-001-873-11
; Sequence 11, Application US/10001873
; Patent No. US20020160388A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Heive
; APPLICANT: Chen, Sei-Yu
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; APPLICANT: Turner, Leah
; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prot
; FILE REFERENCE: DEX-0275
; CURRENT APPLICATION NUMBER: US/10/001.873
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,055
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: 60/252,496
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 2467
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2319)..(2319)
; OTHER INFORMATION: a, c, g or t
US-10-001-873-11

Query Match 59.7%; Score 265.2; DB 9; Length 2467;
Best Local Similarity 78.1%; Pred. No. 2.1e-75;
Matches 345; Conservative 0; Mismatches 93; Indels 4; Gaps 2;

QY 6 GGGCTGCTGATCTGGGGTCT 65
Db 1 GGCTCTCATTTGTTGGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 59
QY 66 GAGATGTGACCTGGCAGAACTCTGAAGAACTTGAGCTGAGCGCTATTAAGAGTCTAG 125
Db 60 AAGGTGTGAGTTGGCAGAACTCTGAAGAACTTGAGCTGAGCGCTATTAAGAGTCTAG 119
QY 126 CCGGCAAACTGTTGTTGTTGACCAAAATGGGAAAGCACTTATACACAAAAGCTACAA 185
Db 120 CCGGCAAACTGTTGTTGTTGACCAAAATGGGAAAGCACTTATACACAAAAGCTACAA 179
QY 186 CTACAAATCTGAGAGAAAGCACTGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 245
Db 180 CTACAAATCTGAGAGAAAGCACTGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 239

QY 246 GTGTATGATGGAAGAAACCCCTTAATGCACTGACGCTGTGATGATGATGATGATGAT 305
Db 240 GTGTATGATGGAAGAAACCCCTTAATGCACTGACGCTGTGATGATGATGATGATGAT 299
QY 306 AATGAAATGACATGCTTAAGAGCTGTACGCTGTACGCTGTACGCTGTACGCTGTACG 362
Db 300 GCTGCAAGATTAACATGCTGTACGCTGTACGCTGTACGCTGTACGCTGTACGCTGTAC 359
QY 363 AGGATTAACAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 422
Db 360 AGGATTAACAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 419
QY 423 CGTTGAGGTTGCAACCTGTAA 444
Db 420 TGTTCAGGTTGTGAGTGTAA 441

RESULT 8

US-09-871-161-344
; Sequence 344, Application US/09871161
; Publication No. US2003009766A1
; GENERAL INFORMATION:
; APPLICANT: ENDEGE, WILSON O., ET AL.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CCDDA-260XX
; CURRENT APPLICATION NUMBER: US/09/871,161
; CURRENT FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 09/328,111
; PRIOR FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: 60/117,393
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 60/098,639
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 544
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 344
; LENGTH: 657
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(657)
; OTHER INFORMATION: n = A,T,C or G
US-09-871-161-344

Query Match 56.3%; Score 250; DB 9; Length 657;
Best Local Similarity 75.9%; Pred. No. 8.4e-71;
Matches 322; Conservative 0; Mismatches 97; Indels 5; Gaps 1;

QY 14 TTATCTGGGGTCT 73
Db 15 TTGTTCTGGGGTCT 74
QY 74 ACCTTGCCAGAACTCTGAAGAACTTGAGCTGAGCGCTATTAAGAGTCTAGCTGCA 133
Db 75 ACCTTGCCAGAACTCTGAAGAACTTGAGCTGAGCGCTATTAAGAGTCTAGCTGCA 134
QY 134 ACTGTGTTGTTGACCAAAATGGGAAAGCACTTATACACAAAAGCTACAACTACAT 193
Db 135 ACTGTGTTGTTGACCAAAATGGGAAAGCACTTATACACAAAAGCTACAACTACAT 194
QY 194 CTAGAGTGAAGAAAGCACTGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 253
Db 195 CTAGAGTGAAGAAAGCACTGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 254
QY 254 ATGCAAAACCCCTTAATGCACTGACGCTGTGATGATGATGATGATGATGATGATGAT 313
Db 255 ATGCAAAACCCCTTAATGCACTGACGCTGTGATGATGATGATGATGATGATGATGAT 314
QY 314 ATGACATGCTTAAGAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 368
Db 314 ATGACATGCTTAAGAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 368

Db 315 ATACATCGTGATCTGTAGCTTGTGCAAAAANGTTGTCCCGATGATCCACAGGCATT 374
OY 369 TACACCTGGTGGATGAGAAAGTATGTCGAGACCATGACGATAGTGTGA 428
Db 375 AAGACATGGGTGGATGAGAAATGTTGTCAAAACAGATGTCCGACATGTCTAA 434
OY 429 GGGT 432
Db 435 NGGT 438

RESULT 9

US-10-060-036-2544/C
; Sequence 2544, Application US/10060036
; Publication No. US20030073144A1

GENERAL INFORMATION:

APPLICANT: Benson, Darin R.
APPLICANT: Kalos, Michael D.
APPLICANT: Lodes, Michael J.
APPLICANT: Persing, David H.
APPLICANT: Hepler, William T.

APPLICANT: Jiang, Yugu

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.566

CURRENT APPLICATION NUMBER: US/10/060,036

NUMBER OF SEQ ID NOS: 4560

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2544

LENGTH: 606

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE: NAME/KEY: misc_feature

LOCATION: 603

OTHER INFORMATION: n = A,T,C or G

US-10-060-036-2544

Query Match

Best Local Similarity 76.4%; Score 190; DB 9; Length 606;
Matches 259; Conservative 0; Mismatches 76; Indels 4; Gaps 2;

OY 109 GGCTATAGGAGTGCAGCTGCAAACTGTTGTGTTTACCAATGGGAAAGCATTT 168
Db 605 GGTTACAGGGAGATCAGCTTACCAATGATGTGTTTGGCAAT-GGAGAGTGTAC 547
OY 169 AACACAAAAGCTACAACTACATCTAGCAGTGAAGCATGATTATGGATTTTCA 228
Db 546 AACACAGAGCTACAACTACATCTAGCAGTGAAGCATGATTATGGATTTTCA 487
OY 229 ATCAACAGCAATGGTGGTGTATGATGCAAAACCCCTAATGACGTTACGGCTGAT 288
Db 486 ATCAATAGCCGTACGTTGTATGTGCAAAACCCCGAGGAGTTATGCTGTCTAT 427
OY 289 GTATCTCGAGCAATTAATGAAATGACATCGCTAAGCTGTAGCGTGTCAAGCAT 348
Db 426 TTAATCTCGAGTCTTGTGTCAGATTAACATCGCTGATGCTGTACCTGTGCAAGAG 367
OY 349 ATTGTAGTGA--GCAAGCATTACAGCTGGTGGCATGAGAAAGCATTTGTGAGAC 405
Db 366 GTTGTCCGTGATCCACAGCATTTAGAGCATGGTGGCATGAGAAAGCATTTGTGCAAAAC 307
OY 406 CATGACGTACAGCATTTAGCTGTGAGGTTGACCCCTTAA 444
Db 306 AGAGATGCTCGTACGATGTTCAGAGTTGTGAGGTGTA 268

RESULT 10
US-10-046-935-1606/C
; Sequence 1606, Application US/10046935
; Patent No. US20020156011A1
; GENERAL INFORMATION:

APPLICANT: Jiang, Yugu
APPLICANT: Harlocker, Susan L.
APPLICANT: Secretist, Heather
APPLICANT: Wang, Aijun
APPLICANT: Stoik, Tom A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.527C1
CURRENT APPLICATION NUMBER: US/10/046,935
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 2235
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1606
LENGTH: 582
TYPE: DNA
ORGANISM: Homo sapiens
US-10-046-935-1606

Query Match 41.8%; Score 185.4; DB 9; Length 582;
Best Local Similarity 76.5%; Pred. No. 7.4e-50;
Matches 241; Conservative 0; Mismatches 71; Indels 3; Gaps 1;

OY 133 AACTGTTGTTTGGACCAATGGGAAAGCATTTATACACAAAGCTACAACTACAT 192
Db 582 AACTGATGTTGTTGGCCAAATGGAGAGTGTTCACACACAGCATACAACTACAT 523
OY 193 CCTAGCAGTGAACCATGATTTATGGATATTTAGATCAACAGCAATGTTGTTAT 252
Db 522 CTTGAGACAGACACATGATTTATGGATTTTATGATCAATACCCCTACTGTGTAAT 463
OY 253 GATGCAAAACCCCTAATGACGTTGAGCGTGTATCTATCTGACGCAATTAATGAA 312
Db 462 GATGCAAAACCCAGAGAGCATTAATGCTGATTTATCTGACGTTGCTGCA 403
OY 313 AATGATCGCTAAGCTGTAGCTGTGCAAAAGCATATTGCACTGA--GCAAGCAT 369
Db 402 AATGATCGCTGATGATGCTGTGCTGTGCAAAAGAGGTTGCTGCTGATCAACAGG 343
OY 370 ACAGCTGGTGGATGAGAAAGCATTTGAGAGCATGACCATGACGACAGTTAGCTGAG 429
Db 342 AGAGATGGTGGATGAGAAAGCATTTGTCAAAACAGAGATGCTGCTGATGTTCAA 283
OY 430 GGTTCACCTGTAA 444
Db 282 GGTGTGAGGTGTA 268

RESULT 11

US-09-878-178-1606/C
; Sequence 1606, Application US/09878178
; Patent No. US20020177552A1

GENERAL INFORMATION:

APPLICANT: Jiang, Yugu
APPLICANT: Harlocker, Susan L.

APPLICANT: Secretist, Heather

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

FILE REFERENCE: 210121.527

CURRENT APPLICATION NUMBER: US/09/878,178

NUMBER OF SEQ ID NOS: 2237

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1606

LENGTH: 582

TYPE: DNA

ORGANISM: Homo sapien

US-09-878-178-1606

Query Match 41.8%; Score 185.4; DB 9; Length 582;
Best Local Similarity 76.5%; Pred. No. 7.4e-50;
Matches 241; Conservative 0; Mismatches 71; Indels 3; Gaps 1;
OY 133 AACTGTTGTTTGGACCAATGGGAAAGCATTTATACACAAAGCTACAACTACAT 192

Db 582 AACGATGTTGGCAATGAGAGTGTACACACAGAGCTACAACTACAT 523
193 CTAAGCATGAAGCACTGATTTATGGATTTTCAATCAACGCAAAATGGTGTAA 252
Db 522 GCTGGAGACAGAAAGCATGATTTATGGATTTTCAATCAATGCGCTACCTGTAA 463
QY 253 GATGCAAAACCCCTAATGAGTGTGAGCGCTGTATGCTGACGCAATTAAGAA 312
Db 462 GATGCAAAACCCAGAGAGTAAATGCTGTATTTCTGCTGAGTGTGCTGCA 403
QY 313 AATGACATGCTAAGCTGTAGCTGTGCAAAACATATGTCAGTA---GCAAGCATT 369
Db 402 GATGACATGCTGTATGCTGTGCAAAAGAGGCTGTGCTGATCACAAGCATT 343
QY 370 ACAGCGTGGTGCATGAAGATGCTGTGCAAGACAGACAGCTGACAGTACGTTGAG 429
Db 342 AGAGCATGGTGTGCAAGAAATGCTGTGCAAAACAGAGATGCTGATATGTTCAA 283
QY 430 GGTGCAACCTGTAA 444
Db 282 GGTGTGAGCTGTA 268

RESULT 12
US-10-146-502-1606/c
; Sequence 1606, Application US/10146502
; Publication No. US20030069180A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Harlocker, Heather
; APPLICANT: Wang, Aijun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.52762
; CURRENT APPLICATION NUMBER: US/10/146,502
; CURRENT FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2241
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1606
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-146-502-1606

Query Match 41.8%; Score 185.4; DB 9; Length 582;
Best Local Similarity 76.5%; Pred. No. 7.4e-50;
Matches 241; Conservative 0; Mismatches 71; Indels 3; Gaps 1;
QY 133 AACTGTTGTGTTGACCAATGGGAAAGCACTTATTAACAAGCTACAACTACAT 192
Db 582 AACTGATGTGTTGGCCAAATGGGAGAGTGTACACACAGAGCTACAACTACAT 523
QY 193 CTAAGCATGAAGCACTGATTTATGGATTTTCAATCAACGCAAAATGGTGTAA 252
Db 522 GCTGGAGACAGAAAGCATGATTTATGGATTTTCAATCAATGCGCTACCTGTAA 463
QY 253 GATGCAAAACCCCTAATGAGTGTGAGCGCTGTATGCTGACGCAATTAAGAA 312
Db 462 GATGCAAAACCCAGAGAGTAAATGCTGTATTTCTGCTGAGTGTGCTGCA 403
QY 313 AATGACATGCTAAGCTGTAGCTGTGCAAAACATATGTCAGTA---GCAAGCATT 369
Db 402 GATGACATGCTGTATGCTGTGCAAAAGAGGCTGTGCTGATCACAAGCATT 343
QY 370 ACAGCGTGGTGCATGAAGATGCTGTGCAAGACAGACAGCTGACAGTACGTTGAG 429
Db 342 AGAGCATGGTGTGCAAGAAATGCTGTGCAAAACAGAGATGCTGATATGTTCAA 283
QY 430 GGTGCAACCTGTAA 444
Db 282 GGTGTGAGCTGTA 268

Db 282 GGTGTGAGCTGTA 268

RESULT 13
US-09-796-692-8055
; Sequence 8055, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8055
; LENGTH: 367
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (331)
; OTHER INFORMATION: n-A,T,C or G
; NAME/KEY: unsure
; LOCATION: (361)
; OTHER INFORMATION: n-A,T,C or G
US-09-796-692-8055

Query Match 38.9%; Score 172.6; DB 9; Length 367;
Best Local Similarity 75.9%; Pred. No. 8.1e-46;
Matches 227; Conservative 0; Mismatches 69; Indels 3; Gaps 1;
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Db 1 CCAATGGGAGAGGTGTACACACAGAGCTACAACTACATGCTGAGACAGAGCA 60
QY 209 CTGATTTGAGATTTTCAATCAATCAACGCAAAATGGTGTATGATGCAAAACCCCTA 268
Db 61 CTGATTTGAGATTTTCAATCAATCAATGCGCTACGCTGTATGATGCAAAACCCCTA 120
QY 269 ATGAGTTGAGCGCTGTATGATGCTGAGCGCAATTAATGAAGAAATGACATGCTAAG 328
Db 121 GAGAGTTATGCTGTATGCTGATTTTCCGAGAGTGTGCTGCAAGATATGATGCTGATG 180
QY 329 CTGAGCGTGTGCAAGCATTTGTCAGTGA---GCAAGCATTTACAGCCTGGGTGCGAT 385
Db 121 GAGAGTTATGCTGTATGCTGATTTTCCGAGAGTGTGCTGCAAGATATGATGCTGATG 180

Db 181 CTGATCTGTGCAAAAGGGTGTCCGTGATCCACAGCATTAAGCATGGGTGGCAT 240
QY 386 GGAAGATCATTTGTCGACCATGACCTGACAGTTCGTTGAGGTTGCACCTGTAA 444
Db 241 GGAGAAATCGTTGTCAAAACAGAGATGTCCGTGATGTTCAGAGTTGTGGAGTGTAA 299

RESULT 14

US-10-040-862-8055
; Sequence 8055, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013520US
; CURRENT FILING DATE: US/10/040,862
; PRIOR APPLICATION NUMBER: US/10-11-06
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; NUMBER OF SEQ ID NOS: 2001-03-01
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 8055
; LENGTH: 367
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (331)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (361)
; OTHER INFORMATION: n=A,T,C or G
US-10-040-862-8055

Query Match 38.9%; Score 172.6; DB 9; Length 367;
Best Local Similarity 75.9%; Pred. No. 8.1e-46;

Matches 227; Conservative 0; Mismatches 69; Indels 3; Gaps 1;

QY 149 CCAATGGAAGACGTTATTAACAAAGCTACAACTACATCTAGCAGTGAAGA 208
Db 1 CCAATGGAAGACGTTATTAACAAAGCTACAACTACATCTAGCAGTGAAGA 60
QY 209 CTGATTAATGGATATTTACAGATCAACAGCAAAATGTTGTGTATGATGCGCAAAACCCCTA 268

Db 61 CTTATTAATGGATATTTACAGATCAACAGCAAAATGTTGTGTATGATGCGCAAAACCCAG 120
QY 269 ATGACGTTGACGGCTGTCATGATCTGTCGAGGAAATTAATGAAATGACATGCTGAAG 328
Db 121 GAGCACTTAATGCTGTCTCATTTATCTCGAGTGCTTTGCTGCAAGATACATCGCTGATG 180
QY 329 CTGTAGCGTGTGCAAAAGCATATTGTCAGTGA---GCAAGGATTAACGCTGGTGGCAT 385
Db 181 CTGTAGCGTGTGCAAAAGGAGGTTGTCCGTGATCCACAGGATTAAGCATGGTGGCAT 240
QY 386 GGAAGATCATTTGTCGACCATGACCTGACAGTTCGTTGAGGTTGCACCTGTAA 444
Db 241 GGAGAAATCGTTGTCAAAACAGAGATGTCCGTGATGTTCAGAGTTGTGGAGTGTAA 299

RESULT 15

US-10-102-524-791
; Sequence 791, Application US/10102524
; Publication No. US20030109434A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Gaiger, Alexander
; APPLICANT: Gordon, Brian
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.572
; CURRENT APPLICATION NUMBER: US/10/102,524
; NUMBER OF SEQ ID NOS: 2002-03-19
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 791
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 447, 456, 466
; OTHER INFORMATION: n = A,T,C or G
US-10-102-524-791

Query Match 38.9%; Score 172.6; DB 9; Length 522;
Best Local Similarity 75.9%; Pred. No. 9.9e-46;

Matches 227; Conservative 0; Mismatches 69; Indels 3; Gaps 1;

QY 149 CCAATGGAAGACGTTATTAACAAAGCTACAACTACATCTAGCAGTGAAGA 208
Db 1 CCAATGGAAGACGTTATTAACAAAGCTACAACTACATCTAGCAGTGAAGA 60
QY 209 CTGATTAATGGATATTTACAGATCAACAGCAAAATGTTGTGTATGATGCGCAAAACCCCTA 268
Db 61 CTTATTAATGGATATTTACAGATCAACAGCAAAATGTTGTGTATGATGCGCAAAACCCAG 120
QY 269 ATGACGTTGACGGCTGTCATGATCTGTCGAGGAAATTAATGAAATGACATGCTGAAG 328
Db 121 GAGCACTTAATGCTGTCTCATTTATCTCGAGTGCTTTGCTGCAAGATACATCGCTGATG 180
QY 329 CTGTAGCGTGTGCAAAAGCATATTGTCAGTGA---GCAAGGATTAACGCTGGTGGCAT 385
Db 181 CTGTAGCGTGTGCAAAAGGAGGTTGTCCGTGATCCACAGGATTAAGCATGGTGGCAT 240
QY 386 GGAAGATCATTTGTCGACCATGACCTGACAGTTCGTTGAGGTTGCACCTGTAA 444
Db 241 GGAGAAATCGTTGTCAAAACAGAGATGTCCGTGATGTTCAGAGTTGTGGAGTGTAA 299

Search completed: July 5, 2003, 06:16:09
Job time: 133 secs

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OM nucleic - nucleic search, using sw model

Run on: July 5, 2003, 06:13:53 ; Search time 1381 Seconds

(without alignments)
9356.731 Million cell updates/sec

Title: US-09-978-199-1

Perfect score: 444
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Scoring table: OLIGO NWC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
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3: gb_in:*
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31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rtd:*
36: em_htg_mam:*
37: em_htg_vit:*
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39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	444	100.0	459	6 108277	108277 Sequence 2
2	444	100.0	951	4 BOVL52B	M26243 Bovine lyso
3	444	100.0	1060	4 BOVL2YM7A	L23758 Bos taurus
4	439	98.9	964	6 112256	M26241 Bovine lyso
5	437	98.4	909	4 BOVL52A	M26241 Bovine lyso
6	437	98.4	963	6 109315	M26244 Bovine lyso
7	395	89.0	877	4 BOVL52C	M26244 Bovine lyso
8	310	69.8	786	4 BOVL52DA	M26240 Bovine lyso
9	202	45.5	1082	4 BOVL523A	M26242 Bovine lyso
10	165	37.2	10212	4 BOVL50ZMB	M50508 Bos taurus
11	130	29.3	8051	4 BOVL50ZMC	M50509 Bos taurus
12	96	21.6	881	4 SHPL2MB	M32493 Sheep lysoz
13	96	21.6	881	4 SHPL2MC	M32494 Sheep lysoz
14	96	21.6	881	4 SHPL2MA	M32495 Sheep lysoz
15	94	21.2	891	4 SHPL2MB	M32496 Bovine lyso
16	87	19.6	881	4 SHPL2MA	M32492 Sheep lysoz
17	87	19.6	885	4 AXIL2MI	M32499 A. axis, lys
18	80	18.0	873	4 AXIL2M2	M32500 A. axis, lys
19	76	17.1	906	4 BOVL521A	M26240 Bovine lyso
20	76	17.1	12222	4 BOVL50ZMA	M50507 Bos taurus
21	64	14.4	8943	4 BRU19466	U19466 Bos taurus
22	63	14.2	875	4 SHPL2MA	M32496 Sheep lysoz
23	63	14.2	1522	4 BRU19469	U19469 Bos taurus
24	61	13.7	1248	4 BOVL2YM14D	L23756 Bos taurus
25	59	13.3	495	4 OAL2A2	AR170553 Ovis arie
26	56	12.6	2499	4 OAL2B1	AR170556 Ovis arie
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28	52	11.7	875	4 SHPL2MA	M32498 Sheep lysoz
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30	49	11.0	3264	4 BRU19468	U19468 Bos taurus
31	46	10.4	1020	4 BOVL2YM5A	L23757 Bos taurus
32	46	10.4	1529	4 BOVL50ZYM	L19980 Bos taurus
33	46	10.4	12039	4 BRU25810	U25810 Bos taurus
34	43	9.7	680	4 OAL2B2	AR170557 Ovis arie
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36	33	7.4	165	9 CAL2M2	U76935 Colobus arie
37	33	7.4	447	9 CGU76916	U76916 Colobus que
38	32	7.2	165	9 PNLM2	U76942 Pygathrix n
39	32	7.2	165	9 NLIZM2	U76946 Nasalis lar
40	32	7.2	447	9 TOUT6817	U76917 Trachypithe
41	32	7.2	447	9 TOUT6818	U76918 Trachypithe
42	31	7.0	165	9 ANL2M2	U76950 Allenopcheu
43	31	7.0	165	9 EPL2M2	U76957 Erythrocebu
44	31	7.0	165	9 MTL2M2	U76953 Miopithecus
45	31	7.0	447	9 CU076923	U76923 Callithrix

ALIGNMENTS

RESULT 1
LOCUS 108277 459 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 2 from Patent EP 0374913.
ACCESSION 108277
VERSION 108277.1 GI:589012
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 459)
AUTHORS Digan, M.E.
TITLE Pichia pastoris glycerol dehydro-3-phosphate dehydrogenase gene
JOURNAL Patent: EP 0374913-A1 2 27-JUN-1990;
FEATURES Location/Qualifiers

source	1. .459	/organism="unknown"
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ORIGIN		
Query Match	100.0%; Score 444; DB 6; Length 459;	
Best Local Similarity	100.0%; Pred. No. 6,4e-249;	
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
OY	1 ATGAAGCTCTGCTATTATCTGAGGGTTCTCTCTTCTGTGCGTGTGCCAAGCGAAGTGC 60	
DB	7 ATGAAGGCTCTGCTATTATCTGAGGGTTCTCTCTTCTGTGCGTGTGCCAAGCGAAGTGC 66	
OY	61 TTGAGACATGTGAGCTGTGCCAAGACCTGSAAGAACTTGGACCTGGACGGCTATTAAAGGA 120	
DB	67 TTGAGACATGTGAGCTGTGCCAAGACCTGSAAGAACTTGGACCTGGACGGCTATTAAAGGA 126	
OY	121 GTCAGCCCTGGCAAACTGGTGTGTTTGACCAAAATGGGAAGCAGTTATTACACAAAGCT 180	
DB	127 GTCAGCCCTGGCAAACTGGTGTGTTTGACCAAAATGGGAAGCAGTTATTACACAAAGCT 186	
OY	181 ACAAACTTCAATCTCCTAGCAGTGAAGACAGCTATTATGGGATATTTTCAGATCAACAGCAA 240	
DB	187 ACAAACTTCAATCTCCTAGCAGTGAAGACAGCTATTATGGGATATTTTCAGATCAACAGCAA 246	
OY	241 TGGTGGTATATGATGGCAAAACCCCTAATGACAGTGAAGCGCTGCATGATATCTCGACG 300	
DB	247 TGGTGGTATATGATGGCAAAACCCCTAATGACAGTGAAGCGCTGCATGATATCTCGACG 306	
OY	301 GAATTAATGAAAAATGACATGCTAAAGCTGTAGCGTGTGCAAAACATATTGTCAAGTGA 360	
DB	307 GAATTAATGAAAAATGACATGCTAAAGCTGTAGCGTGTGCAAAACATATTGTCAAGTGA 366	
OY	361 CAAGCATTAACGCTGGGTGGCATGCAAAAGTCATTGTGCAGACCATGACGTACAGCT 420	
DB	367 CAAGCATTAACGCTGGGTGGCATGCAAAAGTCATTGTGCAGACCATGACGTACAGCT 426	
OY	421 TACGTTGAGGGTTGCACCCCTGTA 444	
DB	427 TACGTTGAGGGTTGCACCCCTGTA 450	
RESULT 2		
LOCUS	BOVL522B 951 bp mRNA linear MAM 27-APR-1993	
DEFINITION	Bovine lysozyme c isozyme 2b mRNA, complete cds.	
ACCESSION	M26243 J04831 M27182	
VERSION	M26243.1 GI:163316	
KEYWORDS	lysozyme.	
SOURCE	Bovine abomasum, cDNA to mRNA, clone lambda-cBL[12,42].	
ORGANISM	Bos taurus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.	
AUTHORS	1 (bases 1 to 951)	
TITLE	Ircin,D.M. and Wilson,A.C.	
JOURNAL	Multiple cDNA sequences and the evolution of bovine stomach	
MEDLINE	lysozyme	
PUBMED	J. Biol. Chem. 264 (19), 11387-11393 (1989)	
COMMENT	89291894	
FEATURES	2738070	
source	Draft entry and computer-readable sequence for [1] kindly submitted by D.M.Ircin, 23-JUN-1989.	
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	/db_xref="taxon:9913"	
	19..462	
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	73. .459			/product="lysozyme 2b"		
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ORIGIN						
Query Match	100.0%	Score 444:	DB 4:	Length 951:		
Best Local Similarity	100.0%	Pred. No. 6,4e-249:	Mismatches 0:	Indels 0:	Gaps 0:	
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61	TTTGAGAGATGTGAGCTTCCAGAACTGTGAAGAACTTGGACTGACGGCTATAAGGA	120				
79	TTTGAAGATGTGAGCTTCCAGAACTGTGAAGAACTTGGACTGACGGCTATAAGGA	138				
121	GTCAAGCCCTGGAACTGGTGTGTTTGACCAATGGGAAAGCACTTTAACAACAAAGCT	180				
139	GTCAAGCCCTGGAACTGGTGTGTTTGACCAATGGGAAAGCACTTTAACAACAAAGCT	198				
181	ACAAACTCAATCTCTAGCAGTGAAGACACTGATTTATGGATATTTCAATACAGCAA	240				
199	ACAAACTCAATCTCTAGCAGTGAAGACACTGATTTATGGATATTTCAATACAGCAA	258				
241	TGTGTGTATGATGAGCAAAACCCCTAATGCACTTACAGGCTCATGTATCTCGAGC	300				
259	TGTGTGTATGATGAGCAAAACCCCTAATGCACTTACAGGCTCATGTATCTCGAGC	318				
301	GAATTAATGAAAAATGACATGCTTAAAGCTGTAGCGTGTGCCAAGCATATTGTCACTG	360				
319	GAATTAATGAAAAATGACATGCTTAAAGCTGTAGCGTGTGCCAAGCATATTGTCACTG	378				
361	CAAGGCATTACAGCTGGGTGGCATGTGAAAAAGCATATGTGAGAGCCATGACGTCAGCT	420				
379	CAAGGCATTACAGCTGGGTGGCATGTGAAAAAGCATATGTGAGAGCCATGACGTCAGCT	438				
421	TACCTTGAAGGTTGACACCTGTAA	444				
439	TACCTTGAAGGTTGACACCTGTAA	462				
RESULT 3						
BOVLIZYM7A						
LOCUS	BOVLIZYM7A	1060 bp	mRNA	linear	MAM 10-MAR-1994	
DEFINITION	Bos taurus lysozyme 7A mRNA.					
ACCESSION	L23758					
VERSION	L23758.1 GI:387905					
KEYWORDS	lysozyme.					
SOURCE	Bos taurus (cow).					
ORGANISM	Bos taurus					
REFERENCE	Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
AUTHORS	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;					
TITLE	1 (bases 1 to 1060)					
JOURNAL	Takeuchi, K., Irwin, D. M., Gallup, M., Shindrot, E., Kal, H.,					
MEDLINE	Stewart, C. B. and Basbaum, C.					
PUBMED	Multiple cDNA sequences of bovine tracheal lysozyme					
FEATURES	J. Biol. Chem. 268 (36), 27440-27446 (1993)					
SOURCE	8262986					
	Location/Qualifiers					
	1..1060					
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	/cell_type="epithelial/ gland"					
	/tissue_type="trachea"					
	/dev_stage="adult"					
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QY 128 TGGCAAACTGTTGTGTTGACCAATGGAAGACGATTATTAACACAAAAGTACAACT 187

Db 123 TGGCAAACTGTTGTGTTGACCAATGGAAGACGATTATTAACACAAAAGTACAACT 182

QY 188 ACAATCTGAGCTGGAAGACATGATTTATGGATATTTTCAGATCAACAGCAATGGTGT 247

Db 183 ACAATCTGAGCTGGAAGACATGATTTATGGATATTTTCAGATCAACAGCAATGGTGT 242

QY 248 GATATGATGGCAAAACCCCTAATGACATGACGCGCTCATGTATCTCTGACGAGATTAA 307

Db 243 GATATGATGGCAAAACCCCTAATGACATGACGCGCTCATGTATCTCTGACGAGATTAA 302

QY 308 TGGAAATGACATGCTTAAGCTGTAGCTGTGCAAAAGCATATTTGTCAGTACAGCAAGCA 367

Db 303 TGGAAATGACATGCTTAAGCTGTAGCTGTGCAAAAGCATATTTGTCAGTACAGCAAGCA 362

QY 368 TTACAGCTGGGTGGCATGGAAGATCATTTGTGAGACACATGACATGACGATTTACGTTG 427

Db 363 TTACAGCTGGGTGGCATGGAAGATCATTTGTGAGACACATGACATGACGATTTACGTTG 422

QY 428 AGGTTGACACCTGTAA 444

Db 423 AGGTTGACACCTGTAA 439

RESULT 6

LOCUS 109315 963 bp DNA linear PAT 02-DEC-1994

DEFINITION Sequence 1 from Patent WO 8904320.

ACCESSION 109315

VERSION 109315.1 GI:587976

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 963)

AUTHORS Digan,M.E., Harpold,M.M., Lair,S.V., Thill,G.P., Siegel,R.S., Ellis,S.B. and Williams,M.E.

TITLE PRODUCTION OF ANIMAL LYSOZYME c VIA SECRETION FROM PICHIA PASTORIS AND COMPOSITION THEREFOR

JOURNAL Patent: WO 8904320-A 1 18-MAY-1989;

FEATURES

source 1. 963

BASE COUNT 298 a 165 c 200 g 299 t 1 others

ORIGIN

Query Match 98.4%; Score 437; DB 6; Length 963;

Best Local Similarity 100.0%; Pred. No. 8.2e-245;

Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 308 TGGAAATGACATGCTTAAGCTGTAGCGTGTGCAAAAGCATATTTGTCAGTACAGCAAGCA 367

Db 326 TGGAAATGACATGCTTAAGCTGTAGCGTGTGCAAAAGCATATTTGTCAGTACAGCAAGCA 385

QY 368 TTACAGCTGGGTGGCATGGAAGATCATTTGTGAGACACATGACGATTTACGTTG 427

Db 386 TTACAGCTGGGTGGCATGGAAGATCATTTGTGAGACACATGACGATTTACGTTG 445

QY 428 AGGTTGACACCTGTAA 444

Db 446 AGGTTGACACCTGTAA 462

RESULT 7

LOCUS BOVLSZ2C 877 bp mRNA linear MAM 27-APR-1993

DEFINITION Bovine lysozyme c isozyyme 2c mRNA, complete cds.

ACCESSION M26244 J04831 M27183

VERSION M26244.1 GI:163318

KEYWORDS Lysozyme.

SOURCE Bovine abomasum, cDNA to mRNA, clones lambda-cBL[20,36,39].

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 877)

AUTHORS Irwin,D.M. and Wilson,A.C.

TITLE Multiple cDNA sequences and the evolution of bovine stomach lysozyme

JOURNAL J. Biol. Chem. 264 (19), 11387-11393 (1989)

MEDLINE 89291894

PUBMED 2738070

COMMENT Draft entry and computer-readable sequence for [1] kindly submitted by D.M. Irwin, 23-JUN-1989.

FEATURES

source location/Qualifiers

1..877

/organism="Bos taurus"

/db_xref="taxon:9913"

<1..399

/note="Lysozyme 2c precursor"

/codon_start=1

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/db_xref="GI:163318"

/translation="YKGRVPERCELTARTLKLDGKYGVSLANMLCTKWSSEYNTKATNYNPSESDYDGIQFQINSKWCMDGCTPAVAVGCHVCSSELMENDIAKAVACAKHIVSEGITAWVAWMSHCRDHDSVYEGCTL"

<1..9

/note="Lysozyme 2c signal peptide"

/product="Lysozyme 2c"

10..396

/product="Lysozyme 2c"

142 c 181 g 269 t

sig_peptide

mat_peptide

BASE COUNT 285 a 142 c 181 g 269 t

ORIGIN

Query Match 89.0%; Score 395; DB 4; Length 877;

Best Local Similarity 100.0%; Pred. No. 3.8e-220;

Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DEFINITION Bos taurus lysozyme gene (cow 2), complete cds.
 ACCESSION M95098
 VERSION M95098.1 GI:163331
 KEYWORDS Lysozyme; repetitive DNA.
 SOURCE Bos taurus DNA.
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
 1 (bases 1 to 10212)
 Irwin,D.M., White,R.T. and Wilson,A.C.
 Characterization of the cow stomach lysozyme genes: repetitive DNA and concerted evolution
 JOURNAL J. Mol. Evol. 37 (4), 355-366 (1993)
 MEDLINE 94141937
 PUBMED 8308905
 FEATURES
 source location/Qualifiers
 1..10212
 /organism="Bos taurus"
 /db_xref="taxon:9913"
 218..511
 /note="putative"
 /rpt_family="Nla"
 /rpt_type="dispersed"
 2506..8130
 /gene="lysozyme"
 join(2506..2672,3840..4004,6136..6211,7575..8130)
 /gene="lysozyme"
 2506..2672
 /gene="lysozyme"
 /note="putative"
 /number=1
 /label=exon1
 join(2537..2672,3840..4004,6136..6211,7575..7641)
 /gene="lysozyme"
 /codon_start=1
 /product="lysozyme"
 /protein_id="AAC37311.1"
 /db_xref="GI:163332"
 /translation="MKALVILGFLFSLVAQKVERCELARTLKLGIDGKVSLSA
 NMICLTWESSYNTKATNPNPSSSESDYGIPOINSKMCNDGKTNPNAVDCGHSVCSSEL
 MENDIAKAVACAKHIYSEOGITAWMAWAKSHCRDHYSSVVGCTL"
 3840..4004
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 /note="putative"
 /number=2
 /label=exon2
 4113..4238
 /gene="lysozyme"
 /note="putative"
 /rpt_family="Bovine Consensus Sequence (BCS)"
 /rpt_type="dispersed"
 4381..4510
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 /note="putative"
 /rpt_family="BCS"
 /rpt_type="dispersed"
 5585..5868
 /gene="lysozyme"
 /note="putative"
 /rpt_family="Nla"
 /rpt_type="dispersed"
 6136..6211
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 /label=exon3
 7575..8130
 /gene="lysozyme"
 /note="putative"
 /number=4
 /label=exon4
 BASE COUNT 3031 a 1982 c 1909 g 3290 t

ORIGIN
 Query Match 37.2%; Score 165; DB 4; Length 10212;
 Best Local Similarity 100.0%; Pred. No. 4e-85;
 Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 137 GGTGCTGTTGACCAATGGGAAAGCAGTTATACACAAAGCTACAACTACAACTCCTA 196
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 Db 3840 GGTGTGTTGACCAATGGGAAAGCAGTTATACACAAAGCTACAACTACAACTCCTA 3899
 QY 197 GCAGTGAAGCAGCTGATTAATGGATATTTTCAGATCAACAGCAAAATGTTGATATGATG 256
 |||||||
 Db 3900 GCAGTGAAGCAGCTGATTAATGGATATTTTCAGATCAACAGCAAAATGTTGATATGATG 3959
 QY 257 GCAGTGAAGCAGCTGATTAATGGATATTTTCAGATCAACAGCAAAATGTTGATATGATG 301
 |||||||
 Db 3960 GCAGTGAAGCAGCTGATTAATGGATATTTTCAGATCAACAGCAAAATGTTGATATGATG 4004
 RESULT 11
 BOVLYSOZMC
 LOCUS Bos taurus lysozyme gene (cow 3), complete cds. MAM 29-OCT-1993
 DEFINITION Bos taurus lysozyme gene (cow 3), complete cds.
 ACCESSION M95099
 VERSION M95099.1 GI:163333
 KEYWORDS Lysozyme; repetitive DNA.
 SOURCE Bos taurus DNA.
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
 1 (bases 1 to 8051)
 Irwin,D.M., White,R.T. and Wilson,A.C.
 Characterization of the cow stomach lysozyme genes: repetitive DNA and concerted evolution
 JOURNAL J. Mol. Evol. 37 (4), 355-366 (1993)
 MEDLINE 94141937
 PUBMED 8308905
 FEATURES
 source location/Qualifiers
 1..8051
 /organism="Bos taurus"
 /db_xref="taxon:9913"
 716..7755
 /gene="lysozyme"
 join(716..904,2158..2322,4118..4193,7192..7755)
 /gene="lysozyme"
 716..904
 /gene="lysozyme"
 /note="putative"
 /number=1
 /label=exon1
 join(769..904,2158..2322,4118..4193,7192..7258)
 /gene="lysozyme"
 /codon_start=1
 /product="lysozyme"
 /protein_id="AAC37312.1"
 /db_xref="GI:163334"
 /translation="MKALVILGFLFSLVAQKVERCELARTLKLGIDGKVSLSA
 NMICLTWESSYNTKATNPNPSSSESDYGIPOINSKMCNDGKTNPNAVDCGHSVCSSEL
 MENDIAKAVACAKHIYSEOGITAWMAWAKSHCRDHYSSVVGCTL"
 2158..2322
 /gene="lysozyme"
 /product="lysozyme"
 /note="putative"
 /label=exon2
 3645..3771
 /gene="lysozyme"
 /note="putative"
 /rpt_family="Bovine Consensus Sequence (BCS)"
 /rpt_type="dispersed"
 4118..4193
 /gene="lysozyme"
 /product="lysozyme"

/note="putative"
/label=exon3
4352..4625
/gene="lysozyme"
/note="putative"
/rpl_family="BCS dimer"
/rpl_type="dispersed"
5308..6746
/gene="lysozyme"
/note="putative"
/rpl_family="Art2 plus approx 900 bp unique"
/rpl_type="dispersed"
7192..7755
/gene="lysozyme"
/note="putative"
/number=4
/label=exon4

BASE COUNT 2412 a 1453 c 1457 g 2729 t

ORIGIN

Query Match 29.3%; Score 130; DB 4; Length 8051;
Best Local Similarity 100.0%; Pred. No. 1.4e-64;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 GGTGGTTGACCAATGGGAAGCAGTTATACACAAAGCTACCAATCAATCTTA 196
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Db 2158 GGTGGTTGACCAATGGGAAGCAGTTATACACAAAGCTACCAATCAATCTTA 2217
|||||

QY 197 GCAGTGAAGCACTGATTTGGATTTTCAGATCAACGCAAAATGGTGTATGATG 256
|||||
Db 2218 GCAGTGAAGCACTGATTTGGATTTTCAGATCAACGCAAAATGGTGTATGATG 2277
|||||

QY 257 GCAGCAACCCC 266
|||||
Db 2278 GCAGCAACCCC 2287
|||||

RESULT 12
SHP12M1B 881 bp mRNA linear MAM 27-APR-1993
LOCUS
DEFINITION Sheep lysozyme 1b (Lzmb1b) mRNA, 3' end.
ACCESSION M32493.1
VERSION M32493.1 GI:165965
KEYWORDS lysozyme 1b.
SOURCE Sheep abomasum, cDNA to mRNA.
ORGANISM Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Caprinae; Ovis.
REFERENCE 1 (bases 1 to 881)
AUTHORS Irwin,D.M. and Wilson,A.C.
TITLE Concerted evolution of ruminant stomach lysozymes. Characterization
of lysozyme cDNA clones from sheep and deer
J. Biol. Chem. 265 (9), 4944-4952 (1990)
JOURNAL 90202968
MEDLINE 2318875
PUBMED

COMMENT Draft entry and computer-readable sequence for [1] kindly submitted
by D.M.Irwin, 01-MAR-1990.

FEATURES
source location/Qualifiers
1..881
/organism="Ovis aries"
/db_xref="taxon:9940"
<1..390
/note="lysozyme 1b precursor"
/codon_start=1
/protein_id="AA31558.1"
/db_xref="GI:165965"
/translation="KPERCELARTLKEIGLDYKGVSLANWLCTFKWESSYNTKATN
YNPGESESDYGIFOJNSKMWNCNDKTPNAYDCHVSCSELMENNIAKAVACAKHIYSE
OGITAMVAMKSHCRDHDVSSYVEGCSL"
mat_peptide 1..387
misc_feature 1..17

CDS
1..17

/note="PCR primer"
BASE COUNT 285 a 145 c 182 g 269 t

ORIGIN

Query Match 21.6%; Score 96; DB 4; Length 881;
Best Local Similarity 100.0%; Pred. No. 1.3e-44;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 GGACGTGACGGCTATAAGGAGTACGCTGCAAACTGGTTGTTTACCAATGGGAA 159
|||||
Db 46 GGACGTGACGGCTATAAGGAGTACGCTGCAAACTGGTTGTTTACCAATGGGAA 105
|||||

QY 160 AGCAGTTATTAACACAAAGCTACCAATCAATCTT 195
|||||
Db 106 AGCAGTTATTAACACAAAGCTACCAATCAATCTT 141
|||||

RESULT 13
SHP12M1C 881 bp mRNA linear MAM 27-APR-1993
LOCUS
DEFINITION Sheep lysozyme 1c (lyz1c) mRNA, 3' end.
ACCESSION M32494.1
VERSION M32494.1 GI:165967
KEYWORDS lysozyme 1c.
SOURCE Sheep abomasum, cDNA to mRNA.
ORGANISM Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Caprinae; Ovis.
REFERENCE 1 (bases 1 to 881)
AUTHORS Irwin,D.M. and Wilson,A.C.
TITLE Concerted evolution of ruminant stomach lysozymes. Characterization
of lysozyme cDNA clones from sheep and deer
J. Biol. Chem. 265 (9), 4944-4952 (1990)
JOURNAL 90202968
MEDLINE 2318875
PUBMED

COMMENT Draft entry and computer-readable sequence for [1] kindly submitted
by D.M.Irwin, 01-MAR-1990.

FEATURES
source location/Qualifiers
1..881
/organism="Ovis aries"
/db_xref="taxon:9940"
<1..390
/note="lysozyme 1c precursor"
/codon_start=1
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/db_xref="GI:165968"
/translation="KPERCELARTLKEIGLDYKGVSLANWLCTFKWESSYNTKATN
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OGITAMVAMKSHCRDHDVSSYVEGCSL"
mat_peptide 1..387
misc_feature 1..17
/product="lysozyme 1c"
/note="PCR primer"
BASE COUNT 285 a 144 c 183 g 269 t

ORIGIN

Query Match 21.6%; Score 96; DB 4; Length 881;
Best Local Similarity 100.0%; Pred. No. 1.3e-44;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 GGACGTGACGGCTATAAGGAGTACGCTGCAAACTGGTTGTTTACCAATGGGAA 159
|||||
Db 46 GGACGTGACGGCTATAAGGAGTACGCTGCAAACTGGTTGTTTACCAATGGGAA 105
|||||

QY 160 AGCAGTTATTAACACAAAGCTACCAATCAATCTT 195
|||||
Db 106 AGCAGTTATTAACACAAAGCTACCAATCAATCTT 141
|||||

RESULT 14
SHP12M2A 881 bp mRNA linear MAM 27-APR-1993
LOCUS

DEFINITION	Accession	Version	Keywords	Source	Organism	Reference	Authors	Title	Journal	Medline	PubMed	Comment
Sheep lysozyme 2a (lyz2a) mRNA, 3' end.	M32495	J05279	M32495.1 GI:165969	lysozyme 2a.	Sheep abomasum, cDNA to mRNA.		Ovis aries	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;				
1 (bases 1 to 881)												
Irwin,D.M. and Wilson,A.C.												
Concerted evolution of ruminant stomach lysozymes. Characterization												
of lysozyme cDNA clones from sheep and deer												
J. Biol. Chem. 265 (9), 4944-4952 (1990)												
90202968												
2318875												
Draft entry and computer-readable sequence for [1] kindly submitted												
by D.M.Irwin, 01-MAR-1990.												
Location/Qualifiers												
1..881												
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/db_xref="taxon:9940"												
<1..390												
/note="lysozyme 2a precursor"												
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/protein_id="PAA31560.1"												
/db_xref="GI:165970"												
/translation="KVFPERELARTLKELGIDGKGVSLANMLCTFKWESSYNTRKTN												
YNPSESTDYGIQINSMKMCNDKCTPNAVDGCHVSCSALMENDIERAVCAKHVSE												
OGIRAWAMKSHCHDHVSSVSECTL"												
1..387												
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1..17												
/note="PCR primer"												
BASE COUNT 287 a 144 c 183 g 267 t												
ORIGIN												
Query Match 21.6%; Score 96; DB 4; Length 881;												
Best Local Similarity 100.0%; Fied. No. 1.3e-44;												
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;												
OY 100 GGACTGACGCGCTTAAAGGAGTACGCGTGGCAACTGTGTGTTTGACCAATGGGAA 159												
Db 46 GACTTGACGCGCTTAAAGGAGTACGCGTGGCAACTGTGTGTTTGACCAATGGGAA 105												
OY 160 AGCAGTTATTAACACAAAGCTACCAACTACATCTCT 195												
Db 106 AGCAGTTATTAACACAAAGCTACCAACTACATCTCT 141												
RESULT 15												
BOVLSZ1B												
LOCUS BOVLSZ1B 891 bp mRNA linear MAM 27-APR-1993												
DEFINITION Bovine lysozyme c isozyme 1b mRNA, complete cds.												
ACCESSION M26246 J04831 M27179												
VERSION M26246.1 GI:163312												
KEYWORDS lysozyme.												
SOURCE Bovine abomasum, cDNA to mRNA, clones lambda-cBL[3,4,35].												
ORGANISM Bos taurus												
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;												
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;												
Bovidae; Bovinae; Bos.												
1 (bases 1 to 891)												
Irwin,D.M. and Wilson,A.C.												
Multiple cDNA sequences and the evolution of bovine stomach												

Query Match	Best Local Similarity	100.0%	Score 444;	DB 24;	Length 444;
Matches 444;	Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGAAGCTCTCGTATTATCTGGGGTTCTCTCTCTCTGTCGTGTCGAAGCAAGGTC	60		
Db	1	ATGAAGGCTCTCGTATTATCTGGGGTTCTCTCTCTCTGTCGTGTCGAAGCAAGGTC	60		
QY	61	TTTGAGAGATGTGAGCTTGCCAGAACTGTGAAGAACTTGAGACTGAGGGCTATTAAGGA	120		
Db	61	TTTGAGAGATGTGAGCTTGCCAGAACTGTGAAGAACTTGAGACTGAGGGCTATTAAGGA	120		
QY	121	GTCAGCTTCGCAAACTGCTGTGTGTTGACCAATGGGAAGACGTTATPACCAAAAAGCT	180		
Db	121	GTCAGCTTCGCAAACTGCTGTGTGTTGACCAATGGGAAGACGTTATPACCAAAAAGCT	180		
QY	181	ACAAACTTCATATCCAGAGTGAAGAAAGCACTGATTTATGGGATATTTCAGATCAACGCAAA	240		
Db	181	ACAAACTTCATATCCAGAGTGAAGAAAGCACTGATTTATGGGATATTTCAGATCAACGCAAA	240		
QY	241	TGCTGCTTAATGATGGCAAAACCCCTATATCAGTTGAACGGCTGTCATGTATCTCGACG	300		
Db	241	TGCTGCTTAATGATGGCAAAACCCCTATATCAGTTGAACGGCTGTCATGTATCTCGACG	300		
QY	301	GAATTAAATGAAAAATGACATGCGTTAAAGCTGTAGCGTGTGCAAAAGCATATTGTCAATGAG	360		
Db	301	GAATTAAATGAAAAATGACATGCGTTAAAGCTGTAGCGTGTGCAAAAGCATATTGTCAATGAG	360		
QY	361	CAAGGCAATTAAGCGCTGGGTGGCAATGAAAGTCAATTTGTCAGAGCAATGAGCTGACGAGT	420		
Db	361	CAAGGCAATTAAGCGCTGGGTGGCAATGAAAGTCAATTTGTCAGAGCAATGAGCTGACGAGT	420		
QY	421	TACGTTGAGGGTTCACACCTGTAA 444			
Db	421	TACGTTGAGGGTTCACACCTGTAA 444			

RESULT 2
AAQ05054 standard; DNA: 459 BP.

AAQ05054: 30-OCT-1990 (first entry)

Sequence encoding bovine Lysozyme c2.

KW	GAPDH: Glyceraldehyde-3-phosphate dehydrogenase.
KM	additive homogenous recombination; bovine lysosyme c2; ds.
XX	
OS	Pichia pastoris.
PN	EP374913-A.
XX	
PD	27-JUN-1990.
XX	
PF	21-DEC-1989; 89BP-0123652.
XX	
PR	22-DEC-1988; 88US-0289357.
XX	
PA	(PHIP) PHILLIPS PETROLEUM CO.
XX	
PI	Digan ME;
DR	
XX	
XX	WPI: 1990-195107/26.
PT	
PT	Novel DNA fragments comprising Pichia pastoris GAPDH gene -
PT	its 5'-regulatory region and 3'-transcription termination
PS	sequence.
CC	
CC	Example 10; Table 2; 26pp; English.
CC	
CC	Sequence may be inserted into the DNA of Pichia pastoris at the
CC	GAPDH locus without disrupting the gene activity, transforming
CC	the cell to produce bovine lysosome.
XX	
SQ	Sequence 459 BP; 132 A; 89 C; 119 G; 119 T; 0 other;
	Query Match 100.0%; Score 444; DB 11; Length 459;
	Best Local Similarity 100.0%; Pred. No. 1.2e-222;
	Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 ATGAAGCTCTCGTATTCTGGGGTTTCCTCCTTCTGTCGTGCCAAGCAAGGTC 60
DB	7 ATGAAGGCTCTCGTATTCTGGGGTTTCCTCCTTCTGTCGTGCCAAGCAAGGTC 66
OY	61 TTTGAGAGATGTAGCTTGCAGAACTCTGAAGAACTTGGACTGGACGGCTATAAGGA 120
DB	67 TTTGAGAGATGTAGCTTGCAGAACTCTGAAGAACTTGGACTGGACGGCTATAAGGA 126
OY	121 GTGAGCCGTGGCAAACCTGGTGTGTGACCAAAATGGGAAAGCAGTATTAACAACAAAGCT 180
DB	127 GTGAGCCGTGGCAAACCTGGTGTGTGACCAAAATGGGAAAGCAGTATTAACAACAAAGCT 186
OY	181 ACAAACTCAATCTCAGCAGTAGAAAGCACTGATTTGGATATTTCAGATCAACAGCAAA 240
DB	187 ACAAACTCAATCTCAGCAGTAGAAAGCACTGATTTGGATATTTCAGATCAACAGCAAA 246
OY	241 TGTGGTGTATGATGGCAAAACCCCTAATSCAGTTGACGGCTGTCAATGATTCCTGCAGC 300
DB	247 TGTGGTGTATGATGAGCAAAACCCCTAATGAGATGACGGCTGTCAATGATTCCTGCAGC 306
OY	301 GAATTAATGAAAAATGACATGCTTAAGCTGTAGCGTGTGCAAAAGCATATTGTCAAGTAG 360
DB	307 GAATTAATGAAAAATGACATGCTTAAGCTGTAGCGTGTGCAAAAGCATATTGTCAAGTAG 366
OY	361 CAAGGCATTACAGCTGGGTGGCAATGGAAAGTCATTTGTGAGACCATAGACGTAGAGCT 420
DB	367 CAAGGCATTACAGCTGGGTGGCAATGGAAAGTCATTTGTGAGACCATAGACGTAGAGCT 426
OY	421 TAGCTTGAAGGTTGCACCTGTAA 444
DB	427 TAGCTTGAAGGTTGCACCTGTAA 450
RESULT 3	
ID	AAD39129 standard; DNA: 10130 BP.
XX	
AC	AAD39129;


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QY 6 GGCCTCGTATTCTGGGGTTTCCTTCCTTCTGTCGTCGCAAGGCAAGGCTTTGA 65
DB 24 GGCTCTGCTATTCTGGGGTTTCCTTCCTTCTGTCGTCGCAAGGCTTTGA 83
QY 66 GAGATGTGAGCTTGGCCGAAGACTGGAAGAACTTGGAGCTGAGCGCTATAAGGAGTCAG 125
DB 84 GAGATGTGAGCTTGGCCGAAGACTGGAAGAACTTGGAGCTGAGCGCTATAAGGAGTCAG 143
QY 126 CCTGGCAAACTGGTGTGTTGTTGACCAATGGGAAGCAGTTATTAACCAAAAGCTCAAA 185
DB 144 CCTGGCAAACTGGTGTGTTGTTGACCAATGGGAAGCAGTTATTAACCAAAAGCTCAAA 203
QY 186 CTACATCTAGACAGTGAAGCACTGATTATGGGATTTTTCAGATCAACAGCAATGGTG 245
DB 204 CTACATCTAGACAGTGAAGCACTGATTATGGGATTTTTCAGATCAACAGCAATGGTG 263
QY 246 GTGTAATGATGGCAAAACCCCTAATGATGAGCGCTGATGATATCCGCGAGCAAT 305
DB 264 GTGTAATGATGGCAAAACCCCTAATGATGAGCGCTGATGATATCCGCGAGCAAT 323
QY 306 AATGGAATGACATGCTTAAGCTGAGCTGTCGAAGCATATTTGTCAGTGAAGCAAG 365
DB 324 AATGGAATGACATGCTTAAGCTGAGCTGTCGAAGCATATTTGTCAGTGAAGCAAG 383
QY 366 CATTACAGCTGGGTGTCATGGAAGTCTTTGTCAGACCATGACGTGACAGTACGT 425
DB 384 CATTACAGCTGGGTGTCATGGAAGTCTTTGTCAGACCATGACGTGACAGTACGT 443
QY 426 TGAGGGTTGCACCCCTGTA 444
DB 444 TGAGGGTTGCACCCCTGTA 462

RESULT 5
AAN92057
ID AAN92057 standard; DNA; 964 BP.
XX
AC AAN92057;
DT 07-APR-1990 (first entry)
XX
DE ss sequence of cDNA insert of clone lambda B13 encoding bovine
DE lysozyme C2 together with 3' untranslated region.
XX
KW Bovine lysozyme C2; protein signal sequence; Pinchia pastoris;
KW heterologous protein secretion
XX
OS Bovine.
XX
FH Key Location/Qualifiers
FT misc_feature 1..23
FT misc_feature /*tag- a
FT misc_feature /standard_name= "ECORI Adaptor"
FT misc_feature 942..964
FT misc_feature /*tag- b
FT misc_feature /standard_name= "EcoRI Adaptor"
FT misc_feature 25..462
FT misc_feature /*tag- c
FT misc_feature 68..462
FT misc_feature /*tag- d
FT misc_feature 463..964
FT misc_feature /*tag- e
XX
XX MO8904320-A.
XX
XX 18-MAY-1989.
XX
XX 02-NOV-1988; 88MO-U503907.
XX
XX 02-NOV-1987; 87US-0115940.
XX
XX (SALK ) SALK INST FOR BIOL. STUD.

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XX XX
PI Digan ME, Harpold KM, Lair SV, Thill GP, Siegel RS, Ellis SB;
PI Williams ME;
XX
XX WPI; 1989-165613/22.
DR P-PSDB; MAP92066.
XX
XX Prod. of animal lysozyme C from pinchia pastoris by secretion
PT - consists of P. pastoris promoter and terminator DNA
PT for transcription
XX
XX Pages 26-29; 85pp; English.
XX
XX The 3'-noncoding sequence does not contain a polyadenylation signal or a
XX poly (A)+ tail. The 5'-terminus does not contain the ATG triplet
XX corresponding to the translation initiation codon for the pre-lysozyme C2
XX mRNA. Thus the cDNA insert encodes 16 amino acids amino-terminal to the
XX amino-terminus of the mature protein.
XX
SQ Sequence 964 BP; 298 A; 165 C; 200 G; 301 T; 0 other;

Query Match 98.4%; Score 437; DB 10; Length 964;
Best Local Similarity 100.0%; Pred. No. 5.5e-219;
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTCCTGTTATTCCTGGGGTTTCCTTCCTTCTGTCGTCGCAAGGCAAGGCTTTGAGA 67
DB 26 CTCCTGTTATTCCTGGGGTTTCCTTCCTTCTGTCGTCGTCGCAAGGCAAGGCTTTGAGA 85
QY 68 GATGTGAGCTTGGCCGAAGACTGGAAGAACTTGGAGCTGAGCGCTATAAGGAGTCAG 127
DB 86 GATGTGAGCTTGGCCGAAGACTGGAAGAACTTGGAGCTGAGCGCTATAAGGAGTCAG 145
QY 128 TGGCAAACTGGTGTGTTGTTGACCAATGGGAAGCAGTTATTAACCAAAAGCTCAAACT 187
DB 146 TGGCAAACTGGTGTGTTGTTGACCAATGGGAAGCAGTTATTAACCAAAAGCTCAAACT 205
QY 188 ACAATCTAGACAGTGAAGCACTGATTATGGGATTTTTCAGATCAACAGCAATGGTG 247
DB 206 ACAATCTAGACAGTGAAGCACTGATTATGGGATTTTTCAGATCAACAGCAATGGTG 265
QY 248 GTAATGATGGCAAAACCCCTAATGATGAGCGCTGATGATATCCGCGAGCAAT 307
DB 266 GTAATGATGGCAAAACCCCTAATGATGAGCGCTGATGATATCCGCGAGCAAT 325
QY 308 TGGAAATGACATGCTTAAGCTGTAGCGTGTGCAAAAGCATATTTGTCAGTGAAGCA 367
DB 326 TGGAAATGACATGCTTAAGCTGTAGCGTGTGCAAAAGCATATTTGTCAGTGAAGCA 385
QY 368 TTACAGCTGGGTGTCATGGAAGTCTTTGTCAGACCATGACGTGACAGTACGT 427
DB 386 TTACAGCTGGGTGTCATGGAAGTCTTTGTCAGACCATGACGTGACAGTACGT 445
QY 428 AGGGTTGCACCCCTGTA 444
DB 446 AGGGTTGCACCCCTGTA 462

RESULT 6
AAG39092
ID AAG39092 standard; DNA; 964 BP.
XX
XX AAG39092;
DT 20-JUL-1993 (first entry)
XX
XX Bovine lysozyme c DNA.
XX
XX
XX Bovine lysozyme c; transgenic; plant; resistance; pathogen;
XX gram negative; bacteria; hen egg white lysozyme; potato; tobacco;
XX tomato; carrot; apple; sunflower; petunia; violet; pseudomonas;
XX Agrobacterium; Xanthomonas; Erwinia; Clavibacter; ss.
XX

```

[illegible]

Db	444	TGAGGTTGCACCTGTAA	462
	RESULT 7		
xx	AAAN70944	standard; DNA; 390 BP.	
xx	AAAN70944;		
xx	09-APR-1991	(first entry)	
xx	Sequence encoding mature human lysozyme (HLZ).		
xx	Antibacterial; antiviral; bacteriolytic; phagocytosis; ss.		
xx	Homo sapiens.		
xx	Key	Location/Qualifiers	
xx	mat_peptide	1..390	
xx		/*tag= a	
xx	DE3540075-A.		
xx	14-MAY-1987.		
xx	12-NOV-1985;	85DE-3540075.	
xx	12-NOV-1985;	85DE-3540075.	
xx	(BOEH) BOEHRINGER INGELHEI.		
xx	Sledziwski A, Chlebowicz-Sledziwska E, Swetly P, Adolf G, Wien AT;		
xx	WPI: 1987-136923/20.		
xx	P-PSDB; AAP70596.		
xx	New hybrid plasmids contg. sequences for human lysozyme - useful		
xx	e.g. as antiviral and antibacterial agent, and transformed hosts.		
xx	Claim 6; p2; 18pp; German.		
xx	A cDNA bank was constructed using total RNA isolated from the human		
xx	lymphoma cell line U-937. The bank was tested by hybridising with		
xx	two radio-labeled 17-mer oligonucleotides (equiv. to the AA		
xx	sequences 26-31 and 63-68 of HLZ). Clones isolated were designated		
xx	PHL 1-1; PHL21 and PHL 23 (contg. an approx. 500 bp insert) and		
xx	PHL2 and PHL8 (contg. a 300 bp insert).		
xx	Sequence 390 BP; 113 A; 68 C; 113 G; 96 T; 0 other;		
xx	Query Match	6.8%; Score 30; DB 8; Length 390;	
xx	Best Local Similarity	100.0%; Pred. No. 1.0e-05;	
xx	Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
xx	204	AAGCAGTATATGGATATTTTCAGATCAA	233
xx	150	AAGCAGTATATGGATATTTTCAGATCAA	179
	RESULT 8		
xx	AAAN92054	standard; DNA; 435 BP.	
xx	AAAN92054;		
xx	07-APR-1990	(first entry)	
xx	Sequence of human pre-lysozyme C of placental origin.		
xx	Plasmid pHLZ100; human placental pre-lysozyme C; human milk lysozyme;		
xx	human histiocyte lymphoma cell line U-937 pre-lysozyme C.		
xx	Homo sapiens.		

```

XX Key Location/Qualifiers
FH conflict replace(36, "T")
FT /*tag- a
FT replace(39, "A")
FT /*tag- b
XX MO8904320-A.
XX 18-MAY-1989.
XX 02-NOV-1988; 88WO-US03907.
XX 02-NOV-1987; 87US-0115940.
XX (SALK ) SALK INST FOR BIOL STUD.
XX Digan ME, Harpold MM, Iair SV, Thill GP, Siegel RS, Ellis SB,
XX Williams ME;
XX WPI; 1989-165613/22.
XX WPI; 1989-165613/22.
XX Prodn. of animal lysozyme C from pichia pastoris by secretion
XX - consists of P. pastoris promoter and terminator DNA
XX for transcription
XX Page 56; ; 85bp; English.
XX Sequence contained in plasmid pHLZ100. Apart from the four N-terminal
XX amino acids, it encodes the entire sequence of human pre-lysozyme C of
XX placental origin in addition to a translational stop signal. The mature
XX lysozyme C corresponding to the pre-lysozyme C encoded by AAN92054 has
XX the same AA sequence as human milk lysozyme. AAN92054 differs from the
XX nucleotide sequence of the cDNAs encoding human pre-lysozyme C isolated
XX from human histiocytic lymphoma cell line U-937 (see FT tags a and b).
XX However, these nucleic acid differences do not alter the amino acid
XX sequence.
XX Sequence 435 BP; 118 A; 79 C; 125 G; 113 T; 0 other;
XX
XX Query Match 6.8%; Score 30; DB 10; Length 435;
XX Best Local Similarity 100.0%; Pred. No. 1.6e-05;
XX Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 204 AAGCAGCTATTATGATATTCAGATCAA 233
XX 192 AAGCAGCTATTATGATATTCAGATCAA 221
XX
XX RESULT 9
XX AAD17740
XX ID AAD17740 standard; cDNA; 444 BP.
XX AC AAD17740;
XX DT 10-DEC-2001 (first entry)
XX DE Human macrophage-expressed cDNA #17.
XX
XX Human macrophage-expressed protein; inflammation; angiogenesis; cancer;
XX transplantation; myelodysplastic syndrome; transgenic animal; ischaemia;
XX gene therapy; Crohn's disease; immune disorder; myeloid leukaemia; shock;
XX sepsis; nephritis; genetic disorder; nervous system disease; neuropathy;
XX Alzheimer's disease; Parkinson's disease; Huntington's disease; fibrosis;
XX amyotrophic lateral sclerosis; lymphoid cell disorder; platelet disorder;
XX thrombocytopenia; osteoarthritis; bone degenerative disorder; thrombosis;
XX periodontal disease; osteoporosis; tissue repair; burn; incision; ulcer;
XX lung; liver; severe combined immunodeficiency; SCID; autoimmune disorder;
XX multiple sclerosis; rheumatoid arthritis; allergy; asthma; thrombolytic;
XX coagulation disorder; hereditary disorder; haemophilia; neuroprotective;
XX antibacterial; immunosuppressive; analgesic; vulnerrary; immunostimulant;
XX vaccine; vasotrophic; nootropic; haemostatic; osteopathic; fungicide;
XX antidiabetic; ss.

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```

XX OS Homo sapiens.
XX Key Location/Qualifiers
FH CDS 14..352
FT /*tag- a
FT /*tag- b
FT sig_peptide 14..67
FT mat_peptide 68..349
FT /*tag- c
FT /*product= "Human mature macrophage-expressed protein"
XX WO200164839-A2.
XX 07-SEP-2001.
XX 28-FEB-2001; 2001WO-US06475.
XX 28-FEB-2000; 2000US-0515126.
XX 31-MAR-2000; 2000US-0540217.
XX 11-DEC-2000; 2000US-0235200.
XX (HYSE-) HYSEQ INC.
XX Dedera D, Boyle BJ, Labat I, Strache-crain B, Drmanac RT;
XX Dickson MC, Jones LW, Liu C, Tang YT;
XX WPI; 2001-582152/65.
XX P-PSDB; AAE10592.
XX Novel macrophage-expressed nucleic acids and polypeptides for diagnosis
XX and treatment of inflammatory, autoimmune, neurological, myeloid or
XX lymphoid cell disorders, cancer and for promoting wound healing
XX Claim 1; Page 150; 158pp; English.
XX
XX The present invention relates to an isolated macrophage-expressed cDNA
XX and its protein. The invention is used in gene therapy and in creating
XX transgenic animals. Macrophage-expressed molecule is useful treating
XX inflammatory conditions such as nephritis, Crohn's disease, ischaemia-
XX reperfusion injury, shock, sepsis, immune responses, cancer and myeloid
XX leukaemia and myelodysplastic syndromes. The protein exhibits activity
XX relating to angiogenesis, cytokine, stem cell growth factor activity and
XX activating/inhibin related activities and is involved in proliferation,
XX differentiation and survival of pluripotent and totipotent stem cells
XX and useful for re-engineering damaged or diseased tissues, manufacture
XX of bio-pharmaceuticals, development of bio-sensors and transplantation.
XX The protein is used to manipulate stem cells in culture to give rise to
XX neuroepithelial cells that is used to augment or replace cells damaged
XX by illness, accidental damage or genetic disorders, induces the
XX proliferation of neural cells and regeneration of nerve and brain tissue
XX and is useful for the treatment of central and peripheral nervous system
XX diseases and neuropathies, such as Alzheimer's, Parkinson's disease,
XX Huntington's disease, amyotrophic lateral sclerosis and involved in
XX chemotactic or chemokinetic activity, regulation of haematopoiesis and
XX is useful for treating lymphoid cell disorders, platelet disorders such
XX as thrombocytopenia and osteoporosis, osteoarthritis, bone degenerative
XX disorders or periodontal disease and for regeneration of bone, cartilage,
XX tendon and ligament and in tissue repair, healing of burns, incisions
XX and ulcers. The invention is also useful for gut protection, treatment
XX of lung or liver fibrosis, immune deficiencies and disorders such as
XX severe combined immunodeficiency (SCID), bacterial or fungal infections,
XX autoimmune disorders eg. multiple sclerosis, rheumatoid arthritis,
XX allergies such as asthma or other respiratory problems and is involved
XX in thrombolytic or thrombotic or other respiratory problems and is involved
XX in thrombolytic or thrombotic or other respiratory problems and is involved
XX disorders (hereditary disorders such as haemophilia) or to enhance
XX coagulation and other haemostatic events in treating wounds resulting
XX from trauma, surgery and inhibits the growth, effects biorhythms or
XX circadian cycles of rhythms, fertility of male or female subjects,
XX metabolism, catabolism, anabolism, processing utilisation, storage or
XX elimination of dietary fat, lipid, protein, carbohydrate, vitamins,
XX minerals, provides analgesic effects or other pain reducing effects,

```

CC Immunoglobulin like activity and as an antigen in a vaccine composition
CC to raise an immune response. The present sequence is human macrophage-
CC expressed cDNA.

XX Sequence 444 BP; 122 A; 92 C; 121 G; 109 T; 0 other;

Query Match 6.8%; Score 30; DB 22; Length 444;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 AAGCACTGATTATGGGATATTTCAGATCAA 233
Db 217 AAGCACTGATTATGGGATATTTCAGATCAA 246

RESULT 10
ID AAN70943 standard; DNA; 447 BP.

XX AAN70943;

AC 09-APR-1991 (first entry)

XX Sequence encoding leader or signal peptide and mature human
DE Lipozyme (HLZ).

XX Antibacterial; antiviral; bacteriolytic; phagocytosis; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT mat_peptide 43..432

FT /*tag- a

PN DE3540075-A.

XX 14-MAY-1987.

XX 12-NOV-1985; 85DE-3540075.

XX 12-NOV-1985; 85DE-3540075.

XX (BOEH) BOEHRINGER INGELHEIM.

PI Siedzlewski A, Chlebowicz-Siedzewska E, Swelly P, Adolf G, Wien AT;

DR WPI; 1987-136923/20.

DR P-PSDB; AAP70596.

XX New hybrid plasmids contg. sequences for human Lipozyme - useful

XX e.g. as antiviral and antibacterial agent, and transformed hosts.

XX Claim 5; p2; 18pp; German.

CC A cDNA bank was constructed using total RNA isolated from the human

CC lymphoma cell line U-937. The bank was tested by hybridising with

CC two radio-labeled 17-mer oligonucleotides (equiv. to the AA

CC sequences 26-31 and 63-68 of HLZ). Clones isolated were designated

CC PHL14-1; PHL21 and PHL 23 (contg. an approx. 500 bp insert) and

CC PHL2 and PHL8 (contg. a 300 bp insert).

SQ Sequence 447 BP; 122 A; 81 C; 125 G; 119 T; 0 other;

Query Match 6.8%; Score 30; DB 8; Length 447;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 AAGCACTGATTATGGGATATTTCAGATCAA 233
Db 192 AAGCACTGATTATGGGATATTTCAGATCAA 221

RESULT 11

ABL37496
ID ABL37496 standard; CDNA; 481 BP.

XX ABL37496;

XX 08-APR-2002 (first entry)

XX Human colon tumour antigen polynucleotide SEQ ID NO:1085.

XX Human; colon cancer; colon tumour antigen; cytostatic; vaccine;

XX colon tumour metastatic antigen; diagnosis; gene; ss.

XX Homo sapiens.

XX WO200196388-A2.

XX 20-DEC-2001.

XX 08-JUN-2001; 2001WO-US18557.

XX 09-JUN-2000; 2000US-210899P.

XX 20-FEB-2001; 2001US-270216P.

XX (CORI-) CORIXA CORP.

XX Jiang Y, Harlocker SL, Secrist H;

XX WPI; 2002-114514/15.

XX Novel isolated colon tumor polynucleotide differentially expressed in

XX colon tumor or colon metastatic tumor and polypeptides encoded by them,

XX useful for inhibiting development of cancer in patient -

XX Claim 1; SEQ ID 1085; 105pp; English.

XX ABL36412 to ABL38645 represent human colon tumour antigen cDNA clones (I)

XX CC which were isolated from human colon tumour and colon metastatic tumour

XX CC cDNA libraries. (I) have cytosolic activity and can be used in vaccine

XX CC production. (I) can be used for stimulating and/or expanding T cells

XX CC specific for a tumour protein on contact with the T cells. They are also

XX CC useful for inhibiting the development of cancer in a patient. (I) can be

XX CC used as probes or primers for nucleic acid hybridisation, for preparing

XX CC mutant species primers, or primers for use in genetic constructions. (I)

XX CC can be used in the diagnosis of a colon tumour.

SQ Sequence 481 BP; 127 A; 93 C; 128 G; 131 T; 2 other;

Query Match 6.8%; Score 30; DB 24; Length 481;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 AAGCACTGATTATGGGATATTTCAGATCAA 233
Db 189 AAGCACTGATTATGGGATATTTCAGATCAA 218

RESULT 12
ID AAN70949 standard; CDNA; 490 BP.

XX AAN70949;

XX 09-APR-1991 (first entry)

XX Sequence encoding human Lipozyme (HLZ) on cDNA clone HL14-1.

XX Antibacterial; antiviral; bacteriolytic; phagocytosis; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 19..454

FT /*tag- a

XX DE3540075-A.
 XX
 XX 14-MAY-1987.
 XX
 XX 12-NOV-1985; 85DE-3540075.
 XX
 XX 12-NOV-1985; 85DE-3540075.
 XX
 XX (BOEH) BOEHRINGER INGELHEI.
 XX
 XX Siedziewski A, Chlebiewicz-Siedziewska E, Swelly P, Adolf G, Wien AT;
 XX
 XX WPI; 1987-136923/20.
 XX
 XX P-PSDB; AAP70599.
 XX
 XX New hybrid plasmids contg. sequences for human lysozyme - useful
 XX e.g. as antiviral and antibacterial agent, and transformed hosts.
 XX
 XX PS Disclosure; Fig 4; 18pp; German.
 XX
 XX A CDNA bank was constructed using total RNA isolated from the human
 XX lymphoma cell line U-937. The bank was tested by hybridising with
 XX two radio-labeled 17-mer oligonucleotides (equiv. to the AA
 XX sequences 26-31 and 63-68 of HLZ). Clones isolated were designated
 XX pHU 14-1, pHU21 and pHU 23 (contg. an approx. 500 bp insert) and
 XX pHU2 and pHU8 (contg. a 300 bp insert).
 XX
 XX SQ Sequence 490 BP; 122 A; 100 C; 149 G; 119 T; 0 other;
 XX
 XX Query Match 6.8%; Score 30; DB 8; Length 490;
 XX Best Local Similarity 100.0%; Pred. No. 1.6e-05;
 XX Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 204 AAGCACTGATTTATGGATATTTTCAGATCAA 233
 XX ||||||||||||||||||||||||||||
 XX Db 211 AAGCACTGATTTATGGATATTTTCAGATCAA 240
 XX
 XX RESULT 13
 XX ABL38017/c
 XX ID ABL38017 standard; CDNA; 585 BP.
 XX
 XX AC ABL38017;
 XX
 XX DT 08-APR-2002 (first entry)
 XX
 XX DE Human colon tumour antigen polynucleotide SEQ ID NO:1606.
 XX
 XX KW Human; colon cancer; colon tumour antigen; cytostatic; vaccine;
 XX KW colon tumour metastatic antigen; diagnosis; gene; ss.
 XX
 XX OS Homo sapiens.
 XX
 XX PN WO200196388-A2.
 XX
 XX PD 20-DEC-2001.
 XX
 XX PF 08-JUN-2001; 2001WO-US18557.
 XX
 XX PR 09-JUN-2000; 2000US-210899P.
 XX PR 20-FEB-2001; 2001US-270216P.
 XX
 XX PA (CORI-) CORIXA CORP.
 XX
 XX PI Jiang Y, Harlocker SL, Secrist H;
 XX
 XX DR WPI; 2002-114514/15.
 XX
 XX PT Novel isolated colon tumor polynucleotide differentially expressed in
 XX PT colon tumor or colon metastatic tumor and polypeptides encoded by them,
 XX useful for inhibiting development of cancer in patient -

PS Claim 1; SEQ ID 1606; 105pp; English.
 XX
 XX CC ABL36412 to ABL38645 represent human colon tumour antigen cDNA clones (I)
 XX CC which were isolated from human colon tumour and colon metastatic tumour
 XX CC cDNA libraries. (I) have cytostatic activity and can be used in vaccine
 XX CC production. (I) can be used for stimulating and/or expanding T cells
 XX CC specific for a tumour protein on contact with the T cells. They are also
 XX CC useful for inhibiting the development of cancer in a patient. (I) can be
 XX CC used as probes or primers for nucleic acid hybridisation, for preparing
 XX CC mutant species primers, or primers for use in genetic constructions. (I)
 XX CC can be used in the diagnosis of a colon tumour.
 XX
 XX SQ Sequence 585 BP; 173 A; 123 C; 108 G; 179 T; 2 other;
 XX
 XX Query Match 6.8%; Score 30; DB 24; Length 585;
 XX Best Local Similarity 100.0%; Pred. No. 1.6e-05;
 XX Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 204 AAGCACTGATTTATGGATATTTTCAGATCAA 233
 XX ||||||||||||||||||||||||||||
 XX Db 511 AAGCACTGATTTATGGATATTTTCAGATCAA 482
 XX
 XX RESULT 14
 XX AAA16339
 XX ID AAA16339 standard; DNA; 657 BP.
 XX
 XX AC AAA16339;
 XX
 XX DT 14-JUN-2000 (first entry)
 XX
 XX DE Human colon cancer differentially expressed nucleotide sequence #344.
 XX
 XX KW Colon cancer; detect; differential expression; human; treatment;
 XX KW detect mutation; non-invasive diagnostic method; ds.
 XX
 XX OS Homo sapiens.
 XX
 XX PN WO200012702-A2.
 XX
 XX PD 09-MAR-2000.
 XX
 XX PF 30-AUG-1999; 99WO-US19424.
 XX
 XX PR 31-AUG-1998; 98US-0098639.
 XX PR 27-JAN-1999; 99US-0117393.
 XX
 XX PA (FARB) BAYER CORP.
 XX
 XX PI Endege WO, Steilmann KE, Astle JH, Burgess CC, Carroll E;
 XX PI Catino TJ, Dwiwedi P, Ford DM, Lewis ME, Molino GA, Monahan JE;
 XX PI Schlegel R;
 XX
 XX DR WPI; 2000-256641/22.
 XX
 XX PT Novel nucleic acids and proteins for identifying therapeutic agents
 XX PT useful for treating and diagnosing cancer, especially colon cancer -
 XX
 XX PS Claim 16; Page 263; 345pp; English.
 XX
 XX CC This sequence represents a human nucleotide sequence which is
 XX CC differentially expressed in colon cancer cells compared to the expression
 XX CC levels in normal cells. The nucleotide sequence can be used as a source
 XX CC of primers and probes. The nucleotide sequence is useful for determining
 XX CC the phenotype of a cell by detecting the differential expression of the
 XX CC sequence relative to a normal cell. The probes derived from the sequence
 XX CC can also be used to determine the phenotype of cells in a sample. Probes
 XX CC used to determine the phenotype of a cell. The primers are useful for
 XX CC detecting a mutation in a test nucleotide sequence and also for detecting
 XX CC cancer, preferably colon cancer. Antibodies against the protein encoded
 XX CC by the nucleotide sequence can also be used in a method to detect colon
 XX CC cancer. The diagnostic method is non-invasive and accurate for diagnosing

CC colon cancer at an early stage.
 XX
 SQ Sequence 657 BP; 184 A; 122 C; 158 G; 178 T; 15 other;

Query Match 6.8%; Score 30; DB 21; Length 657;
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 AAGCACTGATTATGATATTCAGATCAA 233
 ||||||||||||||||||||||||||||
 Db 205 AAGCACTGATTATGATATTCAGATCAA 234

||||||||||||||||||||||||||
 Db 516 AAGCACTGATTATGATATTCAGATCAA 487

Search completed: July 5, 2003, 06:20:13
 Job time : 182 secs

RESULT 15
 ABO58989/c
 ID ABO58989 standard; cDNA; 706 BP.
 XX

AC ABO58989;

DT 02-AUG-2002 (first entry)

DE Human colon cancer related nucleotide sequence SEQ ID NO:2684.

KW Human; colon cancer; cancer; tissue profiling; forensic; mapping;
 KW genetic analysis; diagnostic; antisense therapy; gene; ss.

OS Homo sapiens.

PN W0200229086-A2.

PD 11-APR-2002.

PF 02-OCT-2001; 2001WO-US30732.

PR 02-OCT-2000; 2000US-237271P.

PA (PARB) BAYER CORP.

PI Burgess C, Astle JH, Carroll E, Catino TJ, Dwivedi P, Molino GA;
 PI Thiagalingam A, Lewis ME;

DR WPI; 2002-426115/45.

PT New isolated nucleic acid that is differentially expressed in cancer
 PT tissues useful for determining the presence of colon cancer in a cell
 PT or tissue type, and in antisense therapy

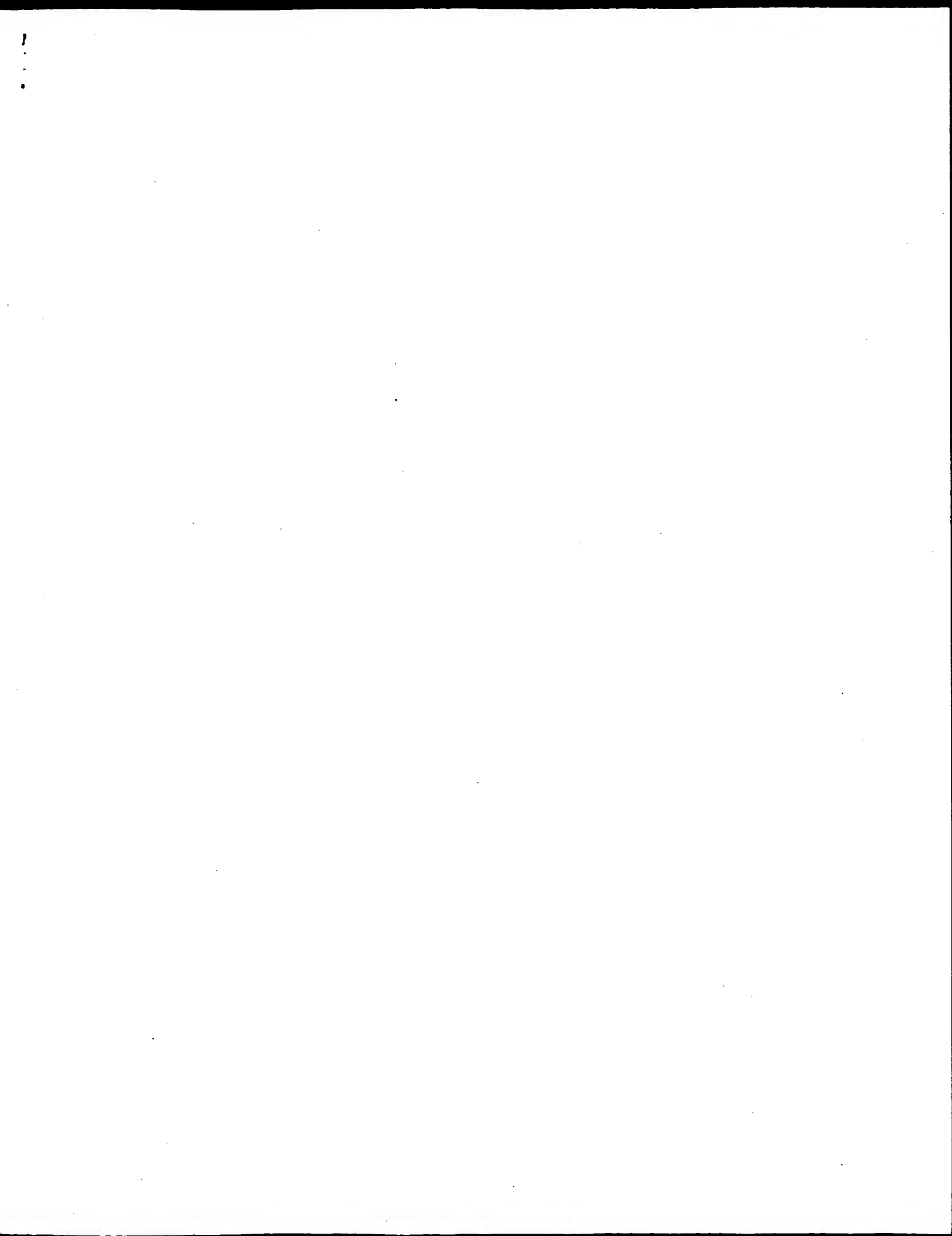
PS Claim 1; Fig 1; 796pp; English.

CC ABO56306 to ABO60787 represent isolated nucleic acids (I) differentially
 CC expressed in cancer tissues. ABB78993 to ABB79004 represent proteins
 CC encoded by the ABO60776 to ABO60787 nucleic acid sequences. (I) can be
 CC used in antisense therapy. An antibody immunoreactive with a polypeptide
 CC encoded by (I) is useful for detecting cancer in a patient sample, and
 CC for detecting the presence or absence of a polynucleotide encoded by a
 CC nucleic acid which hybridizes to (I) in a cell. A probe/primer derived
 CC from (I) can be used for determining the presence of a nucleic acid which
 CC hybridizes to (I), and for determining the phenotype of cells in a sample
 CC of cells from a patient. (I) is useful for determining the presence of
 CC colon cancer in a cell or tissue type, for determining the presence or
 CC state of other type of cancer, in antisense therapy, to generate
 CC microarrays on a solid surface, to identify a chromosome on which the
 CC corresponding gene resides, and in tissue profiling, forensics, genetic
 CC analysis, mapping and diagnostic applications. (I) can be used to raise
 CC antibodies, and to screen for peptide analogues and antagonists.

SQ Sequence 706 BP; 196 A; 156 C; 134 G; 206 T; 14 other;

Query Match 6.8%; Score 30; DB 24; Length 706;
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 AAGCACTGATTATGATATTCAGATCAA 233



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OM nucleic - nucleic search, using sw model

Run on: July 5, 2003, 05:50:38 ; Search time 1138 Seconds
(without alignments)
6318.802 Million cell updates/sec

Title: US-09-978-199-1

Perfect score: 444
Sequence: 1 atgaagctctcgtatctc.....ttgagggttcacacctgtaa 444

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_hiv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_man:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	444	100.0	453	13	BG937925 1AB009H04
2	444	100.0	462	13	BG938107 1AB011D05
3	444	100.0	463	13	BG938377 1AB016E03
4	444	100.0	464	13	BG938413 1AB007G10
5	444	100.0	469	13	BG938112 1AB011D12
6	444	100.0	476	13	BG937589 1AB003C3

7	444	100.0	476	13	BG938203
8	444	100.0	478	13	BG937601 1AB003H1
9	444	100.0	481	13	BG937832 1AB007G03
10	444	100.0	482	13	BG937936 1AB008E01
11	444	100.0	484	13	BG937881 1AB009C06
12	444	100.0	485	13	BG938200 1AB013G04
13	444	100.0	486	13	BG937882 1AB009C07
14	444	100.0	487	13	BG938101 1AB011C10
15	444	100.0	487	13	BG938250 1AB014E01
16	444	100.0	491	13	BG937866 1AB009A09
17	444	100.0	493	13	BG937861 1AB009A04
18	444	100.0	494	13	BG937861 1AB016A01
19	444	100.0	497	13	BG937747 1AB006A06
20	444	100.0	497	13	BG938042 1AB012E07
21	444	100.0	498	13	BG937670 1AB004G05
22	444	100.0	502	13	BG937865 1AB009A08
23	444	100.0	503	13	BG937991 1AB010H03
24	444	100.0	513	13	BG938316 1AB015E06
25	444	100.0	525	10	AW654651 104668 MA
26	444	99.8	448	13	BG937749 1AB006A09
27	439	98.9	448	13	BG938303 1AB015C05
28	439	98.9	484	13	BG938144 1AB008E07
29	438	98.6	453	13	BG937445 1AB013G10
30	437	98.4	456	13	BG9378205 1AB007D02
31	432	97.3	448	13	BG937811 1AB007D02
32	432	97.3	450	13	BG938187 1AB013E09
33	431	97.1	453	13	BG937415 1AB001A08
34	430	96.8	438	13	BG937513 1AB002H02
35	429	96.8	446	13	BG937575 1AB003A6
36	429	96.6	446	13	BG937679 1AB004H07
37	429	96.6	447	13	BG937658 1AB004E08
38	429	96.6	453	13	BG937506 1AB002G01
39	429	96.6	465	13	BG937509 1AB002G04
40	428	96.4	438	13	BG937696 1AB005D04
41	428	96.4	442	13	BG937577 1AB003C6
42	428	96.4	442	13	BG938191 1AB013F01
43	428	96.4	443	13	BG937880 1AB009C05
44	428	96.4	445	13	BG938335 1AB015G08
45	428	96.4	454	13	BG938097 1AB011C03

ALIGNMENTS

RESULT 1
LOCUS 453 bp mRNA linear EST 11-JUN-2001
DEFINITION 1AB009H04 Bovine Abomasum cDNA Library Bos taurus cDNA 5', mRNA
sequence.

ACCESSION BG937925
VERSION BG937925.1 GI:14337297
KEYWORDS
SOURCE

ORGANISM

Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 453)
Moore S.S., Hansen C., Li C., Fu A., Meng Y. and Li G.
CDNA's from bovine abomasum tissue
Unpublished (2001)
Contact: Dr. Stephen Moore
Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
Tel: 780 492 0169
Fax: 780 492 4265
Email: smoores@afns.ualberta.ca

The sequence best matches gb:BV012Y7A (Bos taurus lyszyme 7A mRNA
) in main database at high score of 898.0 and E-value of 0.0
PCR PRIMERS
FORWARD: M13 Forward
REVERSE: M13 Reverse

BACKWARD: M13 Reverse

KEYWORDS	EST.
SOURCE	COW.
ORGANISM	Bos taurus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
AUTHORS	Moore, S.S., Hansen, C., Li, C., Fu, A., Meng, Y. and Li, G.
TITLE	1 (bases 1 to 463)
JOURNAL	CDNA's from bovine abomasum tissue
COMMENT	Unpublished (2001) Contact: Dr. Stephen Moore . Beef Genomics Laboratory Dept of AFNS, University of Alberta 410 Agri/For. Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada Tel: 780 492 0169 Fax: 780 492 4265 Email: smoores@afns.ualberta.ca The sequence best matches gb:BOVLYZM7A (Bos taurus lysozyme 7A mRNA)) In main database at high score of 918.0 and E-value of 0.0 PCR Primers FORWARD: M13 Forward BACKWARD: M13 Reverse Seq primer: T3 primer High quality sequence stop: 463 POLY-A-NO
FEATURES	Location/Qualifiers
Source	1..463 /organism="Bos taurus" /db_xref="taxon:9913" /clone_lib="Bovine Abomasum cDNA Library" /sex="Two males and one female mixed" /tissue_type="Gastrointestinal tissue (GIT)" /cell_type="Epithelial" /dev_stage="Young adult" /lab_host="XL1-BlueMRF"-strain /note="Organ: Abomasum; Vector: Uni-ZAPXR; Site_1: Ecor I; Site_2: Xho I"
BASE COUNT	133 a 91 c 119 g 120 t
ORIGIN	
Query Match	100.0%; Score 444; DB 13; Length 463;
Best Local Similarity	100.0%; Pred. No. 1.5e-223;
Matches	444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 ATGAAGGCTCTGTTATTCCTGGGGTTTCCTCTTCCTTCCTGTCGCTGCCAAGGCAAGGTC 60
DB	20 ATGAAGGCTCTGTTATTCCTGGGGTTTCCTCTTCCTTCCTGTCGCTGCCAAGGCAAGGTC 79
QY	61 TTGGAAGATGTGAGCTGCCAAGACTGTGAAGAACTTGAGAACTTGAGACTGAGAGGCTATTAAGGA 120
DB	80 TTGGAAGATGTGAGCTGCCAAGACTGTGAAGAACTTGAGAACTTGAGAGGCTATTAAGGA 139
QY	121 GTCACCTCGGCAAACTGGTGTGTTGACCAAAATGGAGGAAGCAAGTATTAACAAAAAGCT 180
DB	140 GTCACCTCGGCAAACTGGTGTGTTGACCAAAATGGAGGAAGCAAGTATTAACAAAAAGCT 199
QY	181 ACAAACTACAATCTCAGCAGTGAAGCAAGCACTGTTATGGGATATTTACATCAACAGCAAA 240
DB	200 ACAAACTACAATCTCAGCAGTGAAGCAAGCACTGTTATGGGATATTTACATCAACAGCAAA 259
QY	241 TGGTGGTGAATGATGAGCAAAAACCCCTATGAGTGTGACGGGTGCATGATCTCTGCAGC 300
DB	260 TGGTGGTGAATGATGAGCAAAAACCCCTATGAGTGTGACGGGTGCATGATCTCTGCAGC 319
QY	301 GAATTAATGGAATGATGATGCTTAAGCTGTAGAGGTGCAAAAGCATATTTGTCAGTGAG 360
DB	320 GAATTAATGGAATGATGATGCTTAAGCTGTAGAGGTGCAAAAGCATATTTGTCAGTGAG 379
QY	361 CAAGGCATTTACAGCCTGGGTGTCATGAAAATCTTGTGCAAGCATGAGCTCAGCAGT 420
DB	380 CAAGGCATTTACAGCCTGGGTGTCATGAAAATCTTGTGCAAGCATGAGCTCAGCAGT 439
QY	421 TAGCTTGAAGGTTGCACCTGTAA 444

Db	440	TAGCTTGAGGGGTGCACCCCTGTAA	463
RESULT 4			
BG938413		464 bp	mRNA linear EST 11-JUN-2001
LOCUS			
DEFINITION	1ab007G10	Bovine Abomasum cDNA library	Bos taurus cDNA 5', mRNA
ACCESSION			
VERSION	BG938413.1	GI:14337785	
KEYWORDS			
SOURCE			
ORGANISM			
	Bos taurus		
	Eulayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;		
	Bovidae; Bovinae; Bos.		
	1 (bases 1 to 464)		
	Moore, S.S., Hansen, C., Li, C., Fu, A., Meng, Y., and Li, G.		
	cDNA's from bovine abomasum tissue		
	unpublished (2001)		
	Contact: Dr. Stephen Moore		
	. Beef Genomics Laboratory		
	Dept of AFNS, University of Alberta		
	410 Agri/For. Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada		
	Tel: 780 492 0159		
	Fax: 780 492 4265		
	Email: smoores@atns.ualberta.ca		
	The sequence best matches gb:BOVL2YM7A (Bos taurus lysozyme 7A mRNA		
) in main database at high score of 920.0 and E-value of 0.0		
	PCR primers		
	FORWARD: M13 Forward		
	BACKWARD: M13 Reverse		
	Seq primer: T3 primer		
	POLYA-No.		
FEATURES			
SOURCE			
	Location/Qualifiers		
	1..464		
	/organism="Bos taurus"		
	/db_xref="taxon:9913"		
	/clone_lib="Bovine Abomasum cDNA library"		
	/sex="Two males and one female mixed"		
	/tissue_type="Gastrointestinal tissue (GIT)"		
	/cell_type="Epithelial"		
	/dev_stage="Young adult"		
	/lab_host="XL1-BlueMRF", strain"		
	/note="Organ: Abomasum; Vector: Uni-22APXR; Site_1: EcoR		
	I; Site_2: Xho I"		
BASE COUNT	132 a	92 c	121 g 119 t
ORIGIN			
Query Match	100.0%;	Score 444;	DB 13; Length 464;
Best Local Similarity	100.0%;	Pred. No. 1.5e-223;	
Matches 444;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
1	ATGAAGGCTCCTGATATCTGGGGTTCTCTCTTCCTTGCTGCGTGCACGAAGGTC	60	
14	ATGAAGGCTCCTGATATCTGGGGTTCTCTCTTCCTTGCTGCGTGCACGAAGGTC	73	
61	TTTGAGAGATGTGACCTTGCCAGAACTGGAAGAACTGGACTGGAGGCTATAAGGA	120	
74	TTTGAGAGATGTGACCTTGCCAGAACTGGAAGAACTGGACTGGAGGCTATAAGGA	133	
121	GTGACGCTGGCAAACTGTTGTGTTGTGACCAAAATGGGAAGCAGTTATACACAAAGCT	180	
134	GTGACGCTGGCAAACTGTTGTGTTGTGACCAAAATGGGAAGCAGTTATACACAAAGCT	193	
181	ACAACTCAATCTCAGAGAGTGAAGCACTGATTATGGATTTTCAGATCAACAGCAA	240	
194	ACAACTCAATCTCAGAGAGTGAAGCACTGATTATGGATTTTCAGATCAACAGCAA	253	
241	TGTTGGTGAATGATGGCAAAACCCCTATGAGAGTGAAGCGCTCATGATATCTGCAGC	300	
254	TGTTGGTGAATGATGGCAAAACCCCTATGAGAGTGAAGCGCTCATGATATCTGCAGC	313	

QY	301	GAATTAATGAAAAATGACATCGCTTAAACCTTACCGTGTCGCAAGCATATTGCACTAG	360
Dd	314	GAATTAATGAAAAATGACATCGCTTAAACCTTACCGTGTCGCAAGCATATTGCACTAG <td>373</td>	373
QY	361	CAAGGATTAACACCGCTGGCTGGCATGAAAGCTATTGTGAGACCATGACGTACCACT	420
Dd	374	CAAGGATTAACACCGCTGGCTGGCATGAAAGCTATTGTGAGACCATGACGTACCACT	433
QY	421	TACGTTGAGGGTTGCACCCCTGTAA	444
Dd	434	TACGTTGAGGGTTGCACCCCTGTAA	457

RESULT 5	BG938112	469 bp	MRNA	linear	EST 11-JUN-2001
LOCUS	BG938112				
DEFINITION	AB010112	Bovine Abomasum	CDNA Library	Bos taurus	CDNA 5', MRNA
ACCESSION	BG938112	sequence.			
VERSION	BG938112.1	GI:14337484			
KEYWORDS	EST.				
SOURCE	COW.				

ORGANISM
Bos taurus
Eus taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
Bovidae; Bovinae; Bos.
1 (bases 1 to 469)
REFERENCE
Moore, S.S., Hansen, C., Li, C., Fu, A., Meng, Y. and Li, G.
CDNA's from bovine abomasum tissue
TITLE
JOURNAL
Unpublished (2001)
COMMENT
Contact: Dr. Stephen Moore

Dept of AFNS, University of Alberta
410 April/Fort, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
Tel: 780 492 0165
Fax: 780 492 4265
Email: smoores@afns.ualberta.ca
The sequence best matches gb:BOYLZVW7A (bos taurus lysozyme 7A mRNA)
) in main database at high score of 930.0 and E-value of 0.0
PCR Primers
FORWARD: M13 Forward
BACKWARD: M13 Reverse
Seq primer: T3 primer
High quality sequence stop: 469
POLYA-No.

FEATURES		source	
Location/Qualifiers		1..469	
/organism="Bos taurus"			
/db_xref="taxon.9913"			
/clone_lib="Bovine Abomasum cDNA Library"			
/sex="Two males and one female mixed"			
/tissue_type="Gastrointestinal tissue (GIT)"			
/cell_type="Epithelial"			
/dev_stage="Young adult"			
/lab_host="X11-BlueMR"-strain"			
/note="Organ: Abomasum; Vector: Uni-22APXR; Site_1: Ecor I; Site_2: Xho I"			
BASE COUNT	133 a	92 c	123 g
ORIGIN		121 t	

Query Match:	100.0%;	Score 444;	DB 13;	Length 469;
Best local Similarity	100.0%;	Pred. No. 1.5e-223;		
Matches 444:	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	ATGAAGCCTCGATTATTTGCGGGTTCCTTCTTTCGTGCGCTGCCAAGCAAGGTC	60
Db	17	ATGAAGCCTCGATTATTTGCGGGTTCCTTCTTTCGTGCGCTGCCAAGCAAGGTC	76
QY	61	TTTGAGACATGTGAGCTTTGCCAGACACTCTAAGAACTTGACTGAGCGCTATPAAGGA	120
Db	77	TTTGAGACATGTGAGCTTTGCCAGACACTCTAAGAACTTGACTGAGCGCTATPAAGGA	136

QY	121	GTCAGCCTGGCAAAACGCGTTGTGTTGCACAAAATGGGAACACTTATTAAACAAGAAGCT	180
Dd	137	GTCAGCCTGGCAAAACGCGTTGTGTTGCACAAAATGGGAACACTTATTAAACAAGAAGCT	196
QY	181	ACAACTAACAAATCCTAGCAGTAAGAAGCACCTAATTATGGGATTTTTCAGATCAACAGCAA	240
Dd	197	ACAACTAACAAATCCTAGCAGTAAGAAGCACCTAATTATGGGATTTTTCAGATCAACAGCAA	256
QY	241	TGCTGGTGTAATGATGGCAAAACCCTCATACAGTTGACGGCTGTACATCTCTGACAC	300
Dd	257	TGCTGGTGTAATGATGGCAAAACCCTCATACAGTTGACGGCTGTACATCTCTGACAC	316
QY	301	GATTATATGAAAAATGACATGCGCTAAACCTTACCCTGTGCAAAAGCATATTGTCAGTGAG	360
Dd	317	GATTATATGAAAAATGACATGCGCTAAACCTTACCCTGTGCAAAAGCATATTGTCAGTGAG	376
QY	361	CAAGCATTACACCGCTGGGTGCGACATGAAAAAGTCAATGTGCGAGCACTGACGTACAGCT	420
Dd	377	CAAGCATTACACCGCTGGGTGCGACATGAAAAAGTCAATGTGCGAGCACTGACGTACAGCT	436
QY	421	TACGTTGAGGGTTGCACCCTGTAA	444
Dd	437	TACGTTGAGGGTTGCACCCTGTAA	460

RESULT	6
BG937589	
LOCUS	BG937589
DEFINITION	1AB003C3 Bovine Abomasum cDNA Library Bos taurus cDNA 5' , mRNA
ACCESSION	BG937589
VERSION	BG937589
KEYWORDS	sequence.
SOURCE	BG937589.1 GI:1436961
ORGANISM	EST.
	COW.
	Bos taurus

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 476)	Moore, S.S., Hansen, C., Li, C., Fu, A., Meng, Y. and Li, G.	CDNA's from bovine abomasum tissue	Unpublished (2001)	
	Beef Genomics Laboratory		Contact: Dr. Stephen Moore	
	Dept of AFNS, University of Alberta			
	410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada			
	Tel: 780 492 0169			
	Fax: 780 492 4265			
	Email: smoores@atns.ualberta.ca			
	The sequence best matches gb:BOVIZYW7A (Bos taurus lysozyme 7A mRNA)			
	in main database at high score of 944.0 and E-value of 0.0			
	PCR PRIMERS			
	FORWARD: M13 Forward			
	BACKWARD: M13 Reverse			
	Seq primer: T3 primer			
	High quality sequence stop: 476			
	POLYA-No.			

FEATURES	Location/Qualifiers
source	1..476
	/organism="Bos taurus"
	/db_xref="taxon:9913"
	/clone_lib="Bovine Abomasum cDNA Library"
	/sex="Two males and one female mixed"
	/tissue_type="Gastrointestinal tissue (GIT)"
	/cell_type="Epithelial"
	/dev_stage="Young adult"
	/lab_host="XLI-BlueMRP"-strain"
	/note="Organ: Abomasum; Vector: Uni-22APXR; Site_1: EcoR I; Site_2: Xho I"
BASE COUNT	135 a 94 c 122 g 125 t
ORIGIN	
Query Match	100.0%; Score 444; DB 13; Length 476;

Best Local Similarity 100.0%; Pred. No. 1,5e-223;
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0

OY	1	ATGAAGGCTCCGTTATATCTGGGGTTTCTCTCCCTTCTGCGCGTGTCCAAAGGCAAGGTC	60
Db	6	ATGAAGGCTCCGTTATATCTGGGGTTTCTCTCCCTTCTGCGCGTGTCCAAAGGCAAGGTC	65
OY	61	TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAAGAACTTGGACTGAGCGGCTATAAGGGA	120
Db	66	TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAAGAACTTGGACTGAGCGGCTATAAGGGA	125
OY	121	GTCAGCCCTGGAAACTGGTGTGTGTTTGACCAATATGGGAAAGCAGTTATTAACAAAGCT	180
Db	126	GTCAGCCCTGGAAACTGGTGTGTGTTTGACCAATATGGGAAAGCAGTTATTAACAAAGCT	185
OY	181	ACAAACTCAATCCTAGCAGTGAAGACGCTATTTATGGATATTTTCAGATCAACAGCAAA	240
Db	186	ACAAACTCAATCCTAGCAGTGAAGACGCTATTTATGGATATTTTCAGATCAACAGCAAA	245
OY	241	TGTGTGTATATGATGCCAAACCCCTATATGCAAGTGTGACGGCTGTCATGTATCTGCAGC	300
Db	246	TGTGTGTATATGATGTGGCAAAACCCCTATATGCAAGTGTGACGGCTGTCATGTATCTGCAGC	305
OY	301	GAATTAATGAGAAATGACATGCTTAACCTGTAGCGTGTGCAAAACATATTTGTCAGTGAG	360
Db	306	GAATTAATGAGAAATGACATGCTTAACCTGTAGCGTGTGCAAAACATATTTGTCAGTGAG	365
OY	361	CAAGGCATTAACGCTGGGTGGCATGTGAAAGTCATTGTGAGACCATGACGTCAGCAGT	420
Db	366	CAAGGCATTAACGCTGGGTGGCATGTGAAAGTCATTGTGAGACCATGACGTCAGCAGT	425
OY	421	TACGTTGAGGGTTCACACCTGTAA 444	
Db	426	TACGTTGAGGGTTCACACCTGTAA 449	

RESULT 7	LOCUS	DEFINITION
BG938203	BG938203	476 bp mRNA linear EST 11-JUN-2001
	1AB013608	Bovine Abdomasum cDNA Library Bos taurus cDNA 5', mRNA

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/sex="Two males and one female mixed"
/tissue_type="Gastrointestinal tissue (GIT)"
/cell_type="Epithelial"
/dev_stage="Young adult"
/lab_host="X11-BlueMR"-strain"
/notes="Organ: Abomasum; Vector: Uni-ZAPXR; Site:1: EcoR
I; Site:2: Xho I
93 c 123 g 125 t
135 a
BASE COUNT
ORIGIN

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Query Match	100.0%;	Score 444;	DB 13;	Length 476;
Best Local Similarity	100.0%;	Pred. No. 1.5e-223;		
Matches 444;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

OY	ATGAAGGCTCTGCTTTATCTTTCTGGGGTTTCTCTTCCTTTCTGCGGTGTCGAAGGCAAGTGC	60
Dd	18 ATGAAGGCTCTGCTTTATCTTTCTGGGGTTTCTCTTCCTTTCTGCGGTGTCGAAGGCAAGTGC	77
OY	61 TTTGAGAGATGTGAGCTGTCCAGAACTCTGAAGAACTTGGAGTGGAGCGGCTATTAAGGA	120
Dd	78 TTTGAGAGATGTGAGCTGTCCAGAACTCTGAAGAACTTGGAGTGGAGCGGCTATTAAGGA	137
OY	121 GTGAGCGTGGCAAACTGTTGTGTGTGACCAATGGGAAGACAGTATTAACACAAAAGCT	180
Dd	138 GTGAGCGTGGCAAACTGTTGTGTGTGACCAATGGGAAGACAGTATTAACACAAAAGCT	197
OY	181 ACAAACTACAACTCTAGCAGTGAAAGCACTGATTTATGGATATTTTCAGATCAACAGCAA	240
Dd	198 ACAAACTACAACTCTAGCAGTGAAAGCACTGATTTATGGATATTTTCAGATCAACAGCAA	257
OY	241 TGTGTGTGTATATATGGAACAAACCCCTAATGACATGTACGCGCTGTCATGTCTGTGACG	300
Dd	258 TGTGTGTGTATATATGGAACAAACCCCTAATGACATGTACGCGCTGTCATGTCTGTGACG	317
OY	301 GAATTTATGGAAAAATGACATCGCTTAAAGCTGTAGCGGTGCGAAAGCATATTTGTCAGTGAG	360
Dd	318 GAATTTATGGAAAAATGACATCGCTTAAAGCTGTAGCGGTGCGAAAGCATATTTGTCAGTGAG	377
OY	361 CAAGGATTTACACGCTTGCGGTGGCATGGAAGATCTATTTGCGAGACCATGACGTCAGCAGT	420
Dd	378 CAAGGATTTACACGCTTGCGGTGGCATGGAAGATCTATTTGCGAGACCATGACGTCAGCAGT	437
OY	421 TAGCTTGAGGGTGGACCCCTGTAA 444	
Dd	438 TAGCTTGAGGGTGGACCCCTGTAA 461	

[illegible]

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FEATURES      Location/Qualifiers
              1..476
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                /db_xref="taxon:9913"
                /clone_lib="Bovine Abomasum cDNA Library"
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QY 241 TGGTGTGTATGATGAGCAAAACCCCTAATGACGCTGTGATGATCTGCAGC 300
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 Db 254 TGGTGTGTATGATGAGCAAAACCCCTAATGACGCTGTGATGATCTGCAGC 313
 |||||||
 QY 301 GAATTAATGAAATGACATCGCTAAAGCTGTAGCGTGCAGCAACATATTGTGAGT 360
 |||||||
 Db 314 GAATTAATGAAATGACATCGCTAAAGCTGTAGCGTGCAGCAACATATTGTGAGT 373
 |||||||
 QY 361 CAAGGCAATTAACGCTGTGAGTGAAGAAAGTCATTGTGAGACATGACGTCAGAGT 420
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 Db 374 CAAGGCAATTAACGCTGTGAGTGAAGAAAGTCATTGTGAGACATGACGTCAGAGT 433
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 QY 421 TACGTTGAGGGTTGCACCCCTGTAA 444
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 Db 434 TACGTTGAGGGTTGCACCCCTGTAA 457
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RESULT 12

BG938200

LOCUS 485 bp mRNA linear EST 11-JUN-2001
 DEFINITION 1ABO13G04 Bovine Abomasum cDNA library Bos taurus cDNA 5', mRNA
 ACCESSION BG938200
 VERSION BG938200.1 GI:14337572
 KEYWORDS EST.

SOURCE

ORGANISM

Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.

REFERENCE

1 (bases 1 to 485)
 Moore, S.S., Hansen, C., Li, C., Fu, A., Meng, Y. and Li, G.

AUTHORS Moore, S.S., Hansen, C., Li, C., Fu, A., Meng, Y. and Li, G.
 TITLE cDNA's from bovine abomasum tissue
 JOURNAL Unpublished (2001)
 COMMENT Contact: Dr. Stephen Moore

COMMENT

Dept of AFNS, University of Alberta
 410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
 Tel: 780 492 0169
 Fax: 780 492 4265

Email: smoores@afns.ualberta.ca

The sequence best matches gb:BOVLZY7A (Bos taurus lysozyme 7A mRNA
) in main database at high score of 961.0 and E-value of 0.0

PCR Primers

FORWARD: M13 Forward

BACKWARD: M13 Reverse

Seq primer: T3 primer

High quality sequence stop: 485

POLYA-NO.

Location/Qualifiers

FEATURES

source

1..485

/organism="Bos taurus"

/db_xref="taxon:9913"

/clone.lib="Bovine Abomasum cDNA Library"

/sex="Two males and one female mixed"

/tissue_type="Gastrointestinal tissue (GIT)"

/cell_type="Epithelial"

/dev_stage="Young adult"

/lab_host="X11-BlueMRP"-strain"

/note="Organ: Abomasum; Vector: Uni-ZAPPR; Site_1: Ecor

I; Site_2: Xho I"

BASE COUNT 137 a 97 c 123 g 128 t

ORIGIN

Query Match 100.0%; Score 444; DB 13; Length 485;
 Best Local Similarity 100.0%; Pred. No. 1,6e-223;
 Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 TTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAACTTGAGCTGAGCGCTATTAAGGA 120
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 Db 75 TTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAACTTGAGCTGAGCGCTATTAAGGA 134
 |||||||
 QY 121 GTGAGCTTGCCAGAACTGTTGTGTTGACCAAAATGGGAAAGCAGTTATTAACCAAAAGCT 180
 |||||||
 Db 135 GTGAGCTTGCCAGAACTGTTGTGTTGACCAAAATGGGAAAGCAGTTATTAACCAAAAGCT 194
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 QY 181 ACAAACTCAATCTCAGAGCAAGCAAGCACTGATTTATGGGATTTTCATATCAACAGCAA 240
 |||||||
 Db 195 ACAAACTCAATCTCAGAGCAAGCAAGCACTGATTTATGGGATTTTCATATCAACAGCAA 254
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 QY 241 TGGTGTGTATGATGAGCAAAACCCCTAATGACGCTGTGATGATCTGCAGC 300
 |||||||
 Db 254 TGGTGTGTATGATGAGCAAAACCCCTAATGACGCTGTGATGATCTGCAGC 314
 |||||||
 QY 301 GAATTAATGAAATGACATCGCTAAAGCTGTAGCGTGCAGCAACATATTGTGAGT 360
 |||||||
 Db 315 GAATTAATGAAATGACATCGCTAAAGCTGTAGCGTGCAGCAACATATTGTGAGT 374
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 QY 361 CAAGGCAATTAACGCTGTGAGTGAAGAAAGTCATTGTGAGACATGACGTCAGAGT 420
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 Db 375 CAAGGCAATTAACGCTGTGAGTGAAGAAAGTCATTGTGAGACATGACGTCAGAGT 434
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 QY 421 TACGTTGAGGGTTGCACCCCTGTAA 444
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 Db 435 TACGTTGAGGGTTGCACCCCTGTAA 458
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RESULT 13

BG937882

LOCUS 486 bp mRNA linear EST 11-JUN-2001
 DEFINITION 1ABO09C07 Bovine Abomasum cDNA library Bos taurus cDNA 5', mRNA
 ACCESSION BG937882
 VERSION BG937882.1 GI:14337254
 KEYWORDS EST.

AUTHORS Moore, S.S., Hansen, C., Li, C., Fu, A., Meng, Y. and Li, G.
 TITLE cDNA's from bovine abomasum tissue
 JOURNAL Unpublished (2001)
 COMMENT Contact: Dr. Stephen Moore

COMMENT

Dept of AFNS, University of Alberta
 410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
 Tel: 780 492 0169
 Fax: 780 492 4265

Email: smoores@afns.ualberta.ca

The sequence best matches gb:BOVLZY7A (Bos taurus lysozyme 7A mRNA
) in main database at high score of 963.0 and E-value of 0.0

PCR Primers

FORWARD: M13 Forward

BACKWARD: M13 Reverse

Seq primer: T3 primer

High quality sequence stop: 486

POLYA-NO.

Location/Qualifiers

FEATURES

source

1..486

/organism="Bos taurus"

/db_xref="taxon:9913"

/clone.lib="Bovine Abomasum cDNA Library"

/sex="Two males and one female mixed"

/tissue_type="Gastrointestinal tissue (GIT)"

/cell_type="Epithelial"

/dev_stage="Young adult"

/lab_host="X11-BlueMRP"-strain"

/note="Organ: Abomasum; Vector: Uni-ZAPPR; Site_1: Ecor

I; Site_2: Xho I"

BASE COUNT 137 a 97 c 123 g 128 t

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Query Match 100.0%; Score 444; DB 13; Length 485;
 Best Local Similarity 100.0%; Pred. No. 1,6e-223;
 Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN	BASE COUNT	137 a	97 c	124 g	128 t
Query Match	100.0%;	Score 444;	DB 13;	Length 486;	
Best Local Similarity	100.0%;	Pred. No. 1, 6e-223;			
Matches 444;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1	ATGAAGCCTCCGTTATTTCTGGGGTTCTCTCCCTTTCTGTCGCTGTCGAAGGAAAGTC	60		
DB	16	ATGAAGCCTCCGTTATTTCTGGGGTTCTCTCCCTTTCTGTCGCTGTCGAAGGAAAGTC	75		
QY	61	TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAACTTGAGCTGGAAGGCTATTAAGGA	120		
DB	76	TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAACTTGAGCTGGAAGGCTATTAAGGA	135		
QY	121	GTCAGCCTTGCAAACTGGTGTCTGTTTACCAAAATGGGAAGCACTTTATACAAAAAGCT	180		
DB	136	GTCAGCCTTGCAAACTGGTGTCTGTTTACCAAAATGGGAAGCACTTTATACAAAAAGCT	195		
QY	181	ACAAACTACATACCTTACAGTGAAGACAGTATATGAGATATTTACATCAACAGAAA	240		
DB	196	ACAAACTACATACCTTACAGTGAAGACAGTATATGAGATATTTACATCAACAGAAA	255		
QY	241	TGTTGGTGTATATGATGCGAAAAACCCCTAATGCAATGTAAGCGCTCATGTATCTGACG	300		
DB	256	TGTTGGTGTATATGATGCGAAAAACCCCTAATGCAATGTAAGCGCTCATGTATCTGACG	315		
QY	301	GAATTATATGAAAAATGACATCGCTTAAAGCTGTACGCTGTGCAAGCAATATTTGACGTGAG	360		
DB	316	GAATTATATGAAAAATGACATCGCTTAAAGCTGTACGCTGTGCAAGCAATATTTGACGTGAG	375		
QY	361	CAAGGCATTTACAGCCTGGGTGCGATGGAAGAAAGTCATTGTGAGAACATAGACGTGACAGT	420		
DB	376	CAAGGCATTTACAGCCTGGGTGCGATGGAAGAAAGTCATTGTGAGAACATAGACGTGACAGT	435		
QY	421	TACGTGAGGGGTGACACCTGTAA	444		
DB	436	TACGTGAGGGGTGACACCTGTAA	459		
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LOCUS	1A011C10	Bovine Abomasum cDNA Library Bos taurus cDNA 5', mRNA			
DEFINITION		Sequence.			
ACCESSION	BG938101				
VERSION	BG938101.1	GI:14337473			
KEYWORDS	EST.				
SOURCE					
ORGANISM	Bos taurus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;				
	Bovidae; Bovinae; Bos.				
	1 (bases 1 to 486)				
	Moore,S.S., Hansen,C., Li,C., Fu,A., Meng,Y. and Li,G.				
	cDNA's from bovine abomasum tissue				
	Unpublished (2001)				
	Contact: Dr. Stephen Moore				
	. Beef Genomics Laboratory				
	Dept of AFNS, University of Alberta				
	410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada				
	Tel: 780 492 0169				
	Fax: 780 492 4265				
	Email: smoores@afns.ualberta.ca				
) In main database at high score of 963.0 and E-value of 0.0				
	PCR Primers				
	FORWARD: M13 Forward				
	BACKWARD: M13 Reverse				
	Seq primer: T3 primer				
	High quality sequence stop: 486				
	POLTA-No.				
FEATURES		Location/Qualifiers			

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			/db_xref="taxon:9913"	
			/clone_id="Bovine Abomasum cDNA Library"	
			/sex="Two males and one female mixed"	
			/tissue_type="Gastrointestinal tissue (GIT)"	
			/cell_type="Epithelial"	
			/dev_stage="Young adult"	
			/lab_host="Xrl-blueRF"-strain"	
			/note="Organ: Abomasum; Vector: Uni-ZAPXR; Site_1: Ecor	
			I; Site_2: Xho I"	
BASE COUNT	137 a	96 c	123 g	130 t
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Query Match	100.0%; Score 444;	DB 13:	Length 486;	
Best Local Similarity	100.0%; Pred. No.1.6e-223;			
Matches 444;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Qy	1 ATGAAGCCTCGTATTCCTGGGGTTTCCTTCCTTCGTGCGTCGCACGAAGGTC	60		
Dn	11 ATGAAGCCTCGTATTCCTGGGGTTTCCTTCCTTCGTGCGTCGCACGAAGGTC	70		
Qy	61 TTTAGAGAGTGTGAGCTTGCCAAACTCTGAAGAACTTGGACTGAGAGGCTATTAAAGGA	120		
Dn	71 TTTAGAGAGTGTGAGCTTGCCAAACTCTGAAGAACTTGGACTGAGAGGCTATTAAAGGA	130		
QyS	121 GTCAGCCTGGCAAACTGGTTGTGTTTGACCATAAGGGAACAGTATTAAACAAGCT	180		
Dn	131 GTCAGCCTGGCAAACTGGTTGTGTTTGACCATAAGGGAACAGTATTAAACAAGCT	190		
Qy	181 ACAAACTAACATCTAGCAGTGAAGAAGCATGATTATGGATATTTAGATCAACGAAA	240		
Dn	191 ACAAACTAACATCTAGCAGTGAAGAAGCATGATTATGGATATTTAGATCAACGAAA	250		
Qy	241 TGCGGTGATATATGCGAAAAACCCCTAATGCAATGACGCTGCATGTATCTCGAGC	300		
Dn	251 TGCGGTGATATATGCGAAAAACCCCTAATGCAATGACGCTGCATGTATCTCGAGC	310		
Qy	301 GAATTAATGAAAAATGACATGCTTAAAGCTGTAGCGTGTGCCAAAGCATATTGTCAGTAG	360		
Dn	311 GAATTAATGAAAAATGACATGCTTAAAGCTGTAGCGTGTGTGCAAGCATATTGTCAGTAG	370		
Qy	361 CAAGGCAATACAGCCTGGGTGGCATGTGAAAAAGTATTTGCAAGCAATGAGCTACAGCT	420		
Dn	371 CAAGGCAATACAGCCTGGGTGGCATGTGAAAAAGTATTTGCAAGCAATGAGCTACAGCT	430		
Qy	421 TACGTTGAGGGTTGCACCCCTGTA	444		
Dn	431 TACGTTGAGGGTTGCACCCCTGTA	454		
RESULT 15				
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LOCUS	ABO1E01	Bovine Abomasum cDNA Library	Bos taurus cDNA 5', mRNA	
DEFINITION	Sequence.			
ACCESSION	Bg938250			
VERSION	Bg938250.1	GI:14337622		
KEYWORDS	EST.			
SOURCE				
ORGANISM	Bos taurus			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
	Bovidae; Bovinae; Bos.			
	1 (bases 1 to 487)			
REFERENCE	Moore,S.S., Hansen,C., Li,C., Fu,A., Meng,Y. and Li,G.			
AUTHORS	cDNA's from bovine abomasum tissue			
TITLE	Unpublished (2001)			
JOURNAL	Contact: Dr. Stephen Moore			
COMMENT	. Beef Genomics Laboratory			
	Dept of AFNS, University of Alberta			
	410 Agril/Fort. Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada			
	Tel: 780 492 0169			

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OM nucleic - nucleic search, using sw model

Run on: July 5, 2003, 06:17:08 ; Search time 42 Seconds

(without alignments)
3242.011 Million cell updates/sec

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Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

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Minimum DB seq length: 0

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	439	98.9	964	1	US-07-798-223A-1
2	30	6.8	657	4	US-09-385-982-344
3	19	4.3	2044	1	US-08-071-601-3
4	19	4.3	2044	2	US-08-621-100-3
5	18	4.1	20	1	US-08-071-601-15
6	18	4.1	20	2	US-08-621-100-15
7	17	3.8	1120	3	US-08-851-190-4
8	17	3.8	2017	4	US-09-291-922-21
9	16	3.6	43	1	US-08-071-601-11
10	16	3.6	43	2	US-08-621-100-11
11	16	3.6	180	1	US-08-419-078-7
12	16	3.6	180	1	US-08-726-883-7
13	16	3.6	191	1	US-08-419-078-8
14	16	3.6	191	1	US-08-726-883-8
15	16	3.6	206	1	US-08-419-078-12
16	16	3.6	206	1	US-08-726-883-12
17	16	3.6	238	3	US-08-993-254-1
18	16	3.6	300	1	US-08-419-078-4
19	16	3.6	300	1	US-08-726-883-4
20	16	3.6	474	4	US-09-221-017B-429
21	16	3.6	575	4	US-08-858-207A-157
22	16	3.6	1322	1	US-08-419-078-1
23	16	3.6	1322	1	US-08-726-883-1
24	16	3.6	1803	1	US-08-821-119-18
25	16	3.6	1803	2	US-08-821-119-1
26	16	3.6	2760	4	US-09-198-484-1
27	16	3.6	2923	4	US-09-619-353-9

28	16	3.6	4131	1	US-08-309-512-3	Sequence 3, Appl
29	16	3.6	4131	5	PCT-US92-08756A-3	Sequence 3, Appl
30	16	3.6	5077	2	US-08-687-956A-22	Sequence 22, Appl
31	16	3.6	5130	1	US-08-220-401-1	Sequence 1, Appl
32	16	3.6	5130	1	US-08-437-362-1	Sequence 1, Appl
33	16	3.6	5130	2	US-08-472-809B-8	Sequence 8, Appl
34	16	3.6	6345	2	US-08-472-809B-7	Sequence 7, Appl
35	16	3.6	38584	4	US-09-453-702B-50	Sequence 50, Appl
36	15	3.4	34	4	US-09-151-189-5	Sequence 5, Appl
37	15	3.4	39	3	US-08-865-960-16	Sequence 16, Appl
38	15	3.4	357	4	US-09-134-001C-2435	Sequence 2435, Ap
39	15	3.4	433	4	US-09-397-787-296	Sequence 296, Ap
40	15	3.4	486	4	US-09-134-001C-1740	Sequence 1740, Ap
41	15	3.4	491	1	US-08-133-711-40	Sequence 40, Appl
42	15	3.4	495	4	US-09-134-001C-2480	Sequence 2480, Ap
43	15	3.4	659	4	US-09-328-111-342	Sequence 342, Ap
44	15	3.4	673	4	US-09-040-984-32	Sequence 32, Appl
45	15	3.4	673	4	US-09-123-912-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1
US-07-798-223A-1
; Sequence 1, Application US/07798223A
; Patent No. 5422108
; GENERAL INFORMATION:
; APPLICANT: MIKROV, T. Erik
; APPLICANT: FILZMAURICE, Leona Claire
; TITLE OF INVENTION: Protection of Plants Against Pathogens
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fitch, Even, Tabin & Flannery
; STREET: 135 South LaSalle Street, Suite 900
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/798, 223A
; FILING DATE: 19911125
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/762, 679
; FILING DATE: 19-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 51984
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)552-1311
; TELEFAX: (619)552-0095
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 964 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 25..459
; US-07-798-223A-1
Query Match 98.9%; Score 439; DB 1; Length 964;
Best Local Similarity 100.0%; Pred. No. 1; Se-226;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY	6	GGCAGCTGTAATCTGAGGGTTCTCTCCCTTCTGTGCTGTGCAAGGCAAGGTCCTTGA	65
Db	24	GGCTCTGTTATTTCTGGGGTTTCTCTCTCTTCTGTGCTGTGCAAGGCAAGGTCCTTGA	83
OY	66	GAGATGTGACCTTGCCAGACTCTGTAGAAACCTTGAGTCGACGGCTTAAGGAGTCAG	125
Db	84	GAGATGTGACCTTGCCAGAACTGTAGAAACCTTGAGTCGACGGCTTAAGGAGTCAG	143
OY	126	CTGTGCAAACTGGTTGTGTTTGAACCAATGGGAAAGCAGTTATTAACACAAAAGCTACAA	185
Db	144	CTGTGCAAACTGGTTGTGTTTGAACCAAAAGGAAAGCAGTTATTAACACAAAAGCTACAA	203
OY	186	CTACAATCCTAGACAGTGAAGACAGCATGATTATGGATATTTACAGTCAACAGCAAAATGGTG	245
Db	204	CTACAATCCTAGACAGTGAAGACAGCATGATTATGGATATTTACAGTCAACAGCAAAATGGTG	263
OY	246	GTTGTAATGATGGCAAAACCCCTTAATGACAGTTGACGGCTGTGCATGTATCTTGACGCAATT	305
Db	264	GTTGTAATGATGGCAAAACCCCTTAATGACAGTTGACGGCTGTGCATGTATCTTGACGCAATT	323
OY	306	AATGAAAAATGACATGCTAAAGCGTGTAGCGGTGCAGAAAGATATTTGCAGTAGCAAGG	365
Db	324	AATGAAAAATGACATGCTAAAGCGTGTAGCGGTGCAGAAAGATATTTGCAGTAGCAAGG	383
OY	366	CATTACAGCCTGGGTGGCATGTGAAAAAGTCATTGTGAGAACCATGACGTACGAGTTACGT	425
Db	384	CATTACAGCCTGGGTGGCATGTGAAAAAGTCATTGTGAGAACCATGACGTACGAGTTACGT	443
OY	426	TGAGGGTGCACCCCTGTAA	444
Db	444	TGAGGGTGCACCCCTGTAA	462

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RESULT 2
US-09-385-982-344
: Sequence 344, Application US/09385982
: Patient No. 6262334
:
GENERAL INFORMATION:
: APPLICANT: ENDEGE, WILSON O., ET AL.
: TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
: TITLE OF INVENTION: PRODUCTS: II
: FILE REFERENCE: CCDNA-260XX
: CURRENT APPLICATION NUMBER: US/09/385,982
: EARLIER FILING DATE: 1999-08-30
: EARLIER APPLICATION NUMBER: 09/328,111
: EARLIER FILING DATE: 1999-06-08
: EARLIER APPLICATION NUMBER: 60/117,393
: EARLIER FILING DATE: 1999-01-27
: EARLIER APPLICATION NUMBER: 60/098,639
: EARLIER FILING DATE: 1998-08-31
: NUMBER OF SEQ ID NOS: 544
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 344
: LENGTH: 657
: TYPE: DNA
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ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)...(657)
: OTHER INFORMATION: n - A,T,C or G
US-09-385-982-344

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QY	204	AAGCAGTATATGGGATATTTTCAGATCA	233
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RESULT 3

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US-08-071-601-3/c
Sequence 3, Application US/08071601
Patent No. 5530177

GENERAL INFORMATION:
APPLICANT: ELEC, GREGORY T.
APPLICANT: BREMEL, ROBERT D.
TITLE OF INVENTION: DNA SEQUENCE ENCODING BOVINE
TITLE OF INVENTION: ALPHA-LACTALBUMIN AND METHODS OF USE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDRUS, SCALES, STARKE & SAWALL
STREET: 100 E. WISCONSIN AVE., SUITE 1100
CITY: MILWAUKEE
STATE: WI
COUNTRY: USA
ZIP: 53202-4178

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/071,601
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/744,765
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: F. 3262-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 255-2022
TELEFAX: (608) 255-2182
TELEX: 26832 ANDSTARK
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2044 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: signal peptide coding region
LOCATION: 1943..2043
FEATURE:
NAME/KEY: inherited control region for a-lactalbumin
LOCATION: 1966
FEATURE:
NAME/KEY: putative steroid response element
LOCATION: 1433..1446
FEATURE:
NAME/KEY: RNA polymerase binding region
LOCATION: 1961..1978
US-08-071-601-3

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	Best Local Similarity	100.0%;	Pred. No. 0.91;		
	Matches 19;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Db	2036 CAGCCCTGGGTGCATGGAA	2018			

RESULT 4
US-08-621-100-3/c
; Sequence 3, Application US/08621100
; Patent No. 5850000

APPLICANT: BREMEL, ROBERT D.

TITLE OF INVENTION: DNA SEQUENCE ENCODING BOVINE
TITLE OF INVENTION: ALPHA-LACTALBUMIN AND METHODS OF USE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDRUS, SCALES, STARKE & SAWALL
STREET: 100 E. WISCONSIN AVE., SUITE 1100
CITY: MILWAUKEE
STATE: WI
COUNTRY: USA
ZIP: 53202-4178
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/621,100
FILING DATE: 22-MAR-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/071,601
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: F. 3262-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 255-2022
TELEFAX: (608) 255-2182
TELEX: 26832 ANDSTARK
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2044 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: signal peptide coding region
LOCATION: 1943..2043
FEATURE:
NAME/KEY: inherited control region for a-lactalbumin
LOCATION: 1966
FEATURE:
NAME/KEY: putative steroid response element
LOCATION: 1433..1446
FEATURE:
NAME/KEY: RNA polymerase binding region
LOCATION: 1961..1978
US-08-621-100-3
Query Match 4.3%; Score 19; DB 2; Length 2044;
Best Local Similarity 100.0%; Pred. No. 0.91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 371 CAGCGTGGTGCGCATGGAA 389
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Db 2036 CAGCGTGGTGCGCATGGAA 2018

RESULT 5
US-08-071-601-15
Sequence 15, Application US/08071601
Patent No. 5530177
GENERAL INFORMATION:
APPLICANT: BLECK, GREGORY T.
APPLICANT: BREMEL, ROBERT D.
TITLE OF INVENTION: DNA SEQUENCE ENCODING BOVINE
TITLE OF INVENTION: ALPHA-LACTALBUMIN AND METHODS OF USE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:

ADDRESSEE: ANDRUS, SCALES, STARKE & SAWALL
STREET: 100 E. WISCONSIN AVE., SUITE 1100
CITY: MILWAUKEE
STATE: WI
COUNTRY: USA
ZIP: 53202-4178
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/071,601
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/744,765
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: F. 3262-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 255-2022
TELEFAX: (608) 255-2182
TELEX: 26832 ANDSTARK
INFORMATION FOR SEQ. ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-071-601-15
Query Match 4.1%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 372 AGCGTGGTGCGCATGGAA 389
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Db 1 AGCGTGGTGCGCATGGAA 18

RESULT 6
US-08-621-100-15
Sequence 15, Application US/08621100
Patent No. 5850000
GENERAL INFORMATION:
APPLICANT: BLECK, GREGORY T.
APPLICANT: BREMEL, ROBERT D.
TITLE OF INVENTION: DNA SEQUENCE ENCODING BOVINE
TITLE OF INVENTION: ALPHA-LACTALBUMIN AND METHODS OF USE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDRUS, SCALES, STARKE & SAWALL
STREET: 100 E. WISCONSIN AVE., SUITE 1100
CITY: MILWAUKEE
STATE: WI
COUNTRY: USA
ZIP: 53202-4178
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/621,100
FILING DATE: 22-MAR-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/071,601
FILING DATE:

APPLICATION NUMBER: US/07/744,765
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: F. 3262-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 255-2022
TELEFAX: (608) 255-2182
TELEX: 26832 ANDSTARK
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-621-100-15

Query Match 4.18; Score 18; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 372 AGCCTGGTGGCATGTGGA 389
DB 1 AGCCTGGTGGCATGTGGA 18

RESULT 7
US-08-851-190-4
Sequence 4, Application US/08851190
Patent No. 6074843
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: HUMAN TSC-22-LIKE PROTEIN
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,190
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0285 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1120 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: TONSNOT01
CLONE: 736663

US-08-851-190-4

Query Match 3.88; Score 17; DB 3; Length 1120;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 AACCTGGAAGAACTTG 100
DB 1104 AACCTGGAAGAACTTG 1120

RESULT 8
US-09-291-922-21
Sequence 21, Application US/09291922
Patent No. 6383776
GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Hiltz, Bill
APPLICANT: Kinney, Tony
APPLICANT: Tingey, Scott
TITLE OF INVENTION: Plant Sugar Transport Proteins
FILE REFERENCE: BB-1163
CURRENT APPLICATION NUMBER: US/09/291,922
CURRENT FILING DATE: 1999-04-14
EARLIER APPLICATION NUMBER: 60/083,044
EARLIER FILING DATE: April 24, 1998
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Microsoft Office 97
SEQ ID NO 21
LENGTH: 2017
TYPE: DNA
ORGANISM: Oryza sativa
US-09-291-922-21

Query Match 3.88; Score 17; DB 4; Length 2017;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 CTGTGCTGTCCAGGC 54
DB 1413 CTGTGCTGTCCAGGC 1429

RESULT 9
US-08-071-601-11
Sequence 11, Application US/08071601
Patent No. 5530177
GENERAL INFORMATION:
APPLICANT: BLECK, GREGORY T.
APPLICANT: BREMEL, ROBERT D.
TITLE OF INVENTION: DNA SEQUENCE ENCODING BOVINE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDROS, SCALES, STARK & SAWALL
STREET: 100 E. WISCONSIN AVE., SUITE 1100
CITY: MILWAUKEE
STATE: WI
COUNTRY: USA
ZIP: 53202-4178
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/071,601
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/744,765
FILING DATE:
ATTORNEY/AGENT INFORMATION:

NAME: Sara, Charles S
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: F. 3262-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 255-2022
TELEFAX: (608) 255-2182
TELEX: 26832 ANDSTARK
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-071-601-11

Query Match 3.6%; Score 16; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 374 CCTGGTGGCATGGAA 389
DB 22 CCTGGTGGCATGGAA 37

RESULT 10
US-08-621-100-11
Sequence 11, Application US/08621100
Patent No. 385000
GENERAL INFORMATION:
APPLICANT: BLECK, GREGORY T.
APPLICANT: BREMEL, ROBERT D.
TITLE OF INVENTION: DNA SEQUENCE ENCODING BOVINE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDRUS, SCALES, STARK & SMALL
STREET: 100 E. WISCONSIN AVE., SUITE 1100
CITY: MILWAUKEE
STATE: WI
COUNTRY: USA
ZIP: 53202-4178
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/621,100
FILING DATE: 22-MAR-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/071,601
FILING DATE:
APPLICATION NUMBER: US/07/744,765
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: F. 3262-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 255-2022
TELEFAX: (608) 255-2182
TELEX: 26832 ANDSTARK
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-621-100-11

Query Match 3.6%; Score 16; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 374 CCTGGTGGCATGGAA 389
DB 22 CCTGGTGGCATGGAA 37

RESULT 11
US-08-419-078-7
Sequence 7, Application US/08419078
Patent No. 5587306
GENERAL INFORMATION:
APPLICANT: HAWKINS, PHILLIP R.
APPLICANT: SEILHAMER, JEFFREY J.
TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3330 HILLVIEW AVENUE
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/419,078
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LUTHER, BARBARA J.
REGISTRATION NUMBER: 33954
REFERENCE/DOCKET NUMBER: PF0030 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-855-0572
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 180 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
LIBRARY: Human Fetal Endothelial - Stressed
CLONE: 067172
US-08-419-078-7

Query Match 3.6%; Score 16; DB 1; Length 180;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 353 TCAGTGAGCAAGGCAT 368
DB 155 TCAGTGAGCAAGGCAT 170

RESULT 12
US-08-726-883-7
Sequence 7, Application US/08726883
Patent No. 5676946
GENERAL INFORMATION:
APPLICANT: HAWKINS, PHILLIP R.
APPLICANT: SEILHAMER, JEFFREY J.
TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3330 HILLVIEW AVENUE
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,883
FILING DATE: 04-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/419,078
FILING DATE: 10-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: LUTHER, BARBARA J.
REGISTRATION NUMBER: 33954
REFERENCE/DOCKET NUMBER: PF0030 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-855-0572
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 180 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
LIBRARY: Human Fetal Endothelial - Stressed
CLONE: 067172
US-08-726-883-7

Query Match 3.6%; Score 16; DB 1; Length 180;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 353 TCAGTGACGACGAT 368
DB 155 TCAGTGACGACGAT 170

RESULT 13
US-08-419-078-8
Sequence 8, Application US/08419078
Patent No. 5587306
GENERAL INFORMATION:
APPLICANT: HAWKINS, PHILLIP R.
APPLICANT: SEILHAMER, JEFFREY J.
TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3330 HILLVIEW AVENUE
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/419,078
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LUTHER, BARBARA J.
REGISTRATION NUMBER: 33954

REFERENCE/DOCKET NUMBER: PF0030 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-855-0572
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
LIBRARY: Human Fetal Endothelial - Stressed
CLONE: 067990
US-08-419-078-8

Query Match 3.6%; Score 16; DB 1; Length 191;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 353 TCAGTGACGACGAT 368
DB 63 TCAGTGACGACGAT 78

RESULT 14
US-08-726-883-8
Sequence 8, Application US/08726883
Patent No. 5676946
GENERAL INFORMATION:
APPLICANT: HAWKINS, PHILLIP R.
APPLICANT: SEILHAMER, JEFFREY J.
TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3330 HILLVIEW AVENUE
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,883
FILING DATE: 04-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/419,078
FILING DATE: 10-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: LUTHER, BARBARA J.
REGISTRATION NUMBER: 33954
REFERENCE/DOCKET NUMBER: PF0030 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-855-0572
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
LIBRARY: Human Fetal Endothelial - Stressed
CLONE: 067990
US-08-726-883-8

Query Match 3.6%; Score 16; DB 1; Length 191;

Best Local Similarity 100.0%; Pred. No. 33;
Matches 16; Conservative 0; Mismatches

0; Indels 0; Gaps 0;

QY 353 TCAGTGAGCAGGCAT 368
|||||
DB 63 TCAGTGAGCAGGCAT 78

RESULT 15

US-08-419-078-12

; Sequence 12, Application US/08419078

; Patent No. 3587306

; GENERAL INFORMATION:

; APPLICANT: HAWKINS, PHILIP R.

; APPLICANT: SEITHAMER, JEFFREY J.

; TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

; STREET: 3330 HILLVIEW AVENUE

; CITY: PALO ALTO

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/419,078

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: LUTHER, BARBARA J.

; REGISTRATION NUMBER: 33954

; REFERENCE/DOCKET NUMBER: PF0030 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-0555

; TELEFAX: 415-855-0572

; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 206 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; IMMEDIATE SOURCE:

; LIBRARY: Inflamed Adenoid

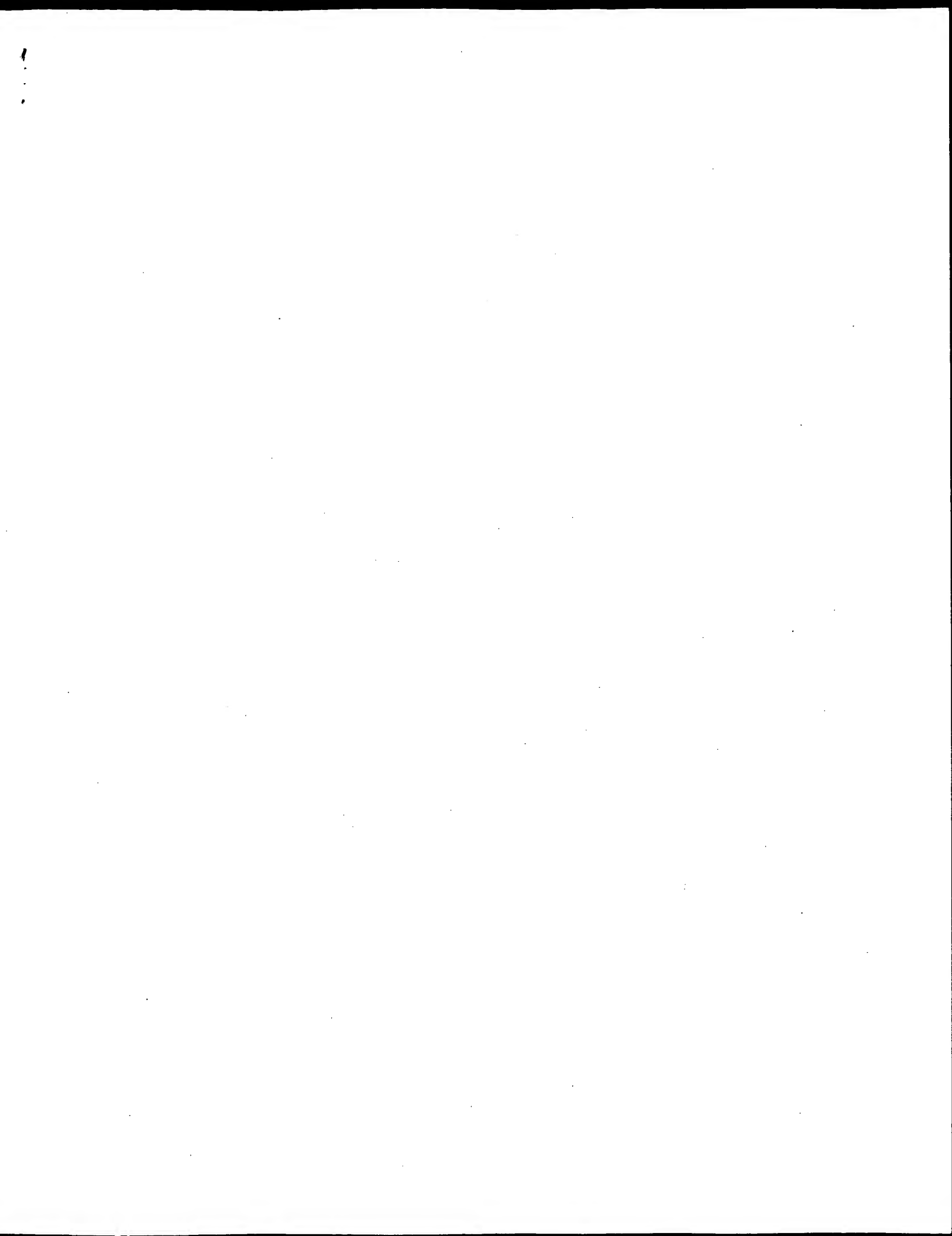
; CLONE: 159363

; US-08-419-078-12

Query Match 3.6%; Score 16; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 353 TCAGTGAGCAGGCAT 368
|||||
DB 72 TCAGTGAGCAGGCAT 87

Search completed: July 5, 2003, 07:05:49
Job time : 43 secs



GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 5, 2003, 06:16:13 ; Search time 131 Seconds
(without alignments)
5290.688 Million cell updates/sec

Title: US-09-978-199-1

Perfect score: 444
Sequence: 1 atgaagcctcgttattct.....ttgagggttgaccctgtaa 444

Scoring table: OLIGO_NTC
Gapop 60.0 , Gapext 60.0

Searched: 1085931 seqs, 780495707 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2171862

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Published Applications - NA: *
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3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq: *
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12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq: *
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq: *
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES:

Result No.	Score	Query Match	Length	ID	Description
1	444	100.0	444	10 US-09-978-199-1	Sequence 1, Appl1
2	444	100.0	10132	10 US-09-978-199-3	Sequence 3, Appl1
3	367	6.8	9	US-09-796-692-8055	Sequence 8055, Ap
4	367	6.8	9	US-10-040-862-8055	Sequence 8055, Ap
5	30	6.8	9	US-10-066-543-3129	Sequence 3129, Ap
6	30	6.8	9	US-10-046-935-1085	Sequence 1085, Ap
7	30	6.8	9	US-09-878-178-1085	Sequence 1085, Ap
8	30	6.8	9	US-10-146-502-1085	Sequence 1085, Ap
9	30	6.8	9	US-10-102-524-791	Sequence 791, App
10	30	6.8	9	US-10-046-935-1606	Sequence 1606, Ap
11	30	6.8	9	US-09-878-178-1606	Sequence 1606, Ap
12	30	6.8	9	US-10-146-502-1606	Sequence 1606, Ap
13	30	6.8	9	US-10-060-036-2544	Sequence 2544, Ap
14	30	6.8	9	US-09-796-692-8226	Sequence 8226, Ap
15	30	6.8	9	US-10-040-862-8226	Sequence 8226, Ap
16	30	6.8	9	US-09-871-161-344	Sequence 344, App
17	30	6.8	10	US-09-969-347-318	Sequence 318, App
18	30	6.8	2467	9 US-10-001-873-11	Sequence 11, Appl
19	23	5.2	479	9 US-10-025-380-526	Sequence 526, App

c 20	23	5.2	479	10 US-09-922-217-526	Sequence 526, App
c 21	23	5.2	479	10 US-09-833-263-526	Sequence 526, App
c 22	23	5.0	34	9 US-09-771-009-34	Sequence 34, Appl
c 23	22	5.0	233	9 US-10-114-666-117	Sequence 117, App
c 24	22	5.0	233	10 US-09-895-828-117	Sequence 117, App
c 25	20	4.5	1125	10 US-09-815-242-6474	Sequence 6474, Ap
c 26	20	4.5	2612	9 US-10-128-714-158	Sequence 158, App
c 27	20	4.5	3087	9 US-10-128-714-158	Sequence 158, App
c 28	19	4.3	30	9 US-09-771-009-35	Sequence 35, Appl
c 29	19	4.3	275	10 US-09-960-352-5019	Sequence 5019, Ap
c 30	19	4.3	284	10 US-09-960-352-290	Sequence 290, App
c 31	19	4.3	4532	10 US-09-930-377B-1	Sequence 1, Appl1
c 32	19	4.3	65359	10 US-09-804-472-3	Sequence 3, Appl1
c 33	17	3.8	40267	9 US-09-978-244A-25	Sequence 25, Appl
c 34	17	3.8	425	9 US-09-918-995-36601	Sequence 36601, A
c 35	17	3.8	680	9 US-09-897-511A-3	Sequence 3, Appl1
c 36	17	3.8	724	10 US-09-897-006-3	Sequence 3, Appl1
c 37	17	3.8	724	9 US-10-171-581-344	Sequence 344, App
c 38	17	3.8	2017	9 US-10-051-902-21	Sequence 21, Appl
c 39	17	3.8	2017	9 US-10-051-902-21	Sequence 21, Appl
c 40	17	3.8	2341	9 US-10-037-270-423	Sequence 423, App
c 41	17	3.8	2745	9 US-09-764-891-5859	Sequence 5859, App
c 42	17	3.8	4207	10 US-09-897-511A-4	Sequence 4, Appl1
c 43	17	3.8	4210	9 US-09-897-006-4	Sequence 4, Appl1
c 44	17	3.8	4210	9 US-09-897-511A-5	Sequence 5, Appl1
c 45	17	3.8	4210	10 US-09-897-006-5	Sequence 5, Appl1

ALIGNMENTS

RESULT 1
US-09-978-199-1
; Sequence 1, Application US/09978199
; Patent No. US20020104126A1
; GENERAL INFORMATION:
; APPLICANT: POGUE, GREGORY P.
; APPLICANT: VELICHKO, SHALENE
; TITLE OF INVENTION: PRODUCTION OF BOVINE LYSOZYME BY PLANT VIRAL VECTORS
; FILE REFERENCE: 42202
; CURRENT FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 60/240,967
; PRIOR FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 444
; TYPE: DNA
; ORGANISM: Bovine sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(441)
US-09-978-199-1

Query Match 100.0%; Score 444; DB 10; Length 444;
Best Local Similarity 100.0%; Pred. No. 1.2e-232;
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGAAGGCTCTGTTATCTGCGGTTTCTCTCTTCTGCGCTGCAAGCAAGTC	60
DB	1	ATGAAGGCTCTGTTATCTGCGGTTTCTCTCTTCTGCGCTGCAAGCAAGTC	60
QY	61	TTTGAAGATGAGCTTCCAGAACTGGAAGAACTGGAAGCAAGTC	120
DB	61	TTTGAAGATGAGCTTCCAGAACTGGAAGAACTGGAAGCAAGTC	120
QY	121	GTCAGCTGCGCAAGCTGTTGTTGACCAATGGAAGCAAGTATTAACCAAACT	180
DB	121	GTCAGCTGCGCAAGCTGTTGTTGACCAATGGAAGCAAGTATTAACCAAACT	180
QY	181	ACAACTACAACTCAGCAAGTAAAGCACTGTTATTTGGATTTCAATCAACGCAA	240
DB	181	ACAACTACAACTCAGCAAGTAAAGCACTGTTATTTGGATTTCAATCAACGCAA	240

Db 181 ACAACATACATCTAGCAGTGAAGACGATGATATTCAGATCAACAGCAA 240
QY 241 TGGTGGTGAATGAGCAAAACCCCTAATGACAGTTCAGCTGATATCTGAGC 300
Db 241 TGGTGGTGAATGAGCAAAACCCCTAATGACAGTTCAGCTGATATCTGAGC 300
QY 301 GAATTAATGAAAAATGACATCGCTAAAGCTGTAGCCGTGTCACAAAGCATATTCAGTGA 360
Db 301 GAATTAATGAAAAATGACATCGCTAAAGCTGTAGCCGTGTCACAAAGCATATTCAGTGA 360
QY 361 CAAGGCATTCACGCTGGGTGGCATGGAAGAAAGCATTTGTGAGACCATGACGTGACAGT 420
Db 361 CAAGGCATTCACGCTGGGTGGCATGGAAGAAAGCATTTGTGAGACCATGACGTGACAGT 420
QY 421 TACGTTGAGGGTTGCACCCCTGTAA 444
Db 421 TACGTTGAGGGTTGCACCCCTGTAA 444

RESULT 2
US-09-978-199-3
; Sequence 3, Application US/09978199
; Patent No. US20020104126A1
; GENERAL INFORMATION:
; APPLICANT: POCHE, GREGORY P.
; APPLICANT: VETICHKO, SHARLENE
; TITLE OF INVENTION: PRODUCTION OF BOVINE LYSOZYME BY PLANT VIRAL VECTORS
; FILE REFERENCE: 42202
; CURRENT APPLICATION NUMBER: US/09/978,199
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 60/240,967
; PRIOR FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 10132
; TYPE: DNA
; ORGANISM: Bovine sp.
US-09-978-199-3

Query Match 100.0%; Score 444; DB 10; Length 10132;
Best Local Similarity 100.0%; Pred. No. 1.3e-232;
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAAGCTCTGCTGTTATTTCTGGGGTTCCTCTCTTCTGTCGCTGCCAAGCAAGTGC 60
Db 5767 ATGAAGCTCTGCTGTTATTTCTGGGGTTCCTCTCTTCTGTCGCTGCCAAGCAAGTGC 5826
QY 61 TTTGAGAGATGAGCTGCTCCAGAACTGGAAGAAACTGAGAGCGCTATTAAGGA 120
Db 5827 TTTGAGAGATGAGCTGCTCCAGAACTGGAAGAAACTGAGAGCGCTATTAAGGA 5886
QY 121 GTACGCTGCAAACTGTTGTGTTGACCAATGGGAAGCAGTTATTAACAAAGCT 180
Db 5887 GTACGCTGCAAACTGTTGTGTTGACCAATGGGAAGCAGTTATTAACAAAGCT 5946
QY 181 ACAAACTAATATCCATGACGATGAAAGCAGCTGATTTATGGGATATTTCAATCAACGCAA 240
Db 5947 ACAAACTAATATCCATGACGATGAAAGCAGCTGATTTATGGGATATTTCAATCAACGCAA 6006
QY 241 TGGTGGTGAATGAGCAAAACCCCTAATGACAGTTCAGCTGATATTCCTGAGC 300
Db 6007 TGGTGGTGAATGAGCAAAACCCCTAATGACAGTTCAGCTGATATTCCTGAGC 6066
QY 301 GAATTAATGAAAAATGACATCGCTAAAGCTGTAGCCGTGTCACAAAGCATATTCAGTGA 360
Db 6067 GAATTAATGAAAAATGACATCGCTAAAGCTGTAGCCGTGTCACAAAGCATATTCAGTGA 6126
QY 361 CAAGGCATTCACGCTGGGTGGCATGGAAGAAAGCATTTGTGAGACCATGACGTGACAGT 420
Db 6127 CAAGGCATTCACGCTGGGTGGCATGGAAGAAAGCATTTGTGAGACCATGACGTGACAGT 6186
QY 421 TACGTTGAGGGTTGCACCCCTGTAA 444

Db 6187 TACGTTGAGGGTTGCACCCCTGTAA 6210

RESULT 3
US-09-796-692-8055
; Sequence 8055, Application US/0996692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Galger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8055
; LENGTH: 367
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (331)
; OTHER INFORMATION: n-A,T,C or G
; NAME/KEY: unsure
; LOCATION: (361)
; OTHER INFORMATION: n-A,T,C or G
US-09-796-692-8055

Query Match 6.8%; Score 30; DB 9; Length 367;
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 204 AAGCAGTATGATGAGATATTCAGATCAA 233
Db 56 AAGCAGTATGATGAGATATTCAGATCAA 85

RESULT 4
US-10-040-862-8055
; Sequence 8055, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Galger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane

```
APPLICANT: Retter, Marc
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
FILE REFERENCE: 014058-013520US
CURRENT APPLICATION NUMBER: US/10/040,862
CURRENT FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: US 60/218,950
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/222,903
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/223,416
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: US 60/223,378
PRIOR FILING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: US 09/796,692
PRIOR FILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 10467
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 8035
LENGTH: 367
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: unsure
LOCATION: (331)
OTHER INFORMATION: n=A,T,C or G
FEATURE:
NAME/KEY: unsure
LOCATION: (361)
OTHER INFORMATION: n=A,T,C or G
US-10-040-862-8035

Query Match 6.8%; Score 30; DB 9; Length 367;
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 AAGCACTGATTATGGATATTTTCAGATCAA 233
DB 56 AAGCACTGATTATGGATATTTTCAGATCAA 85

RESULT 5
US-10-066-543-3129
Sequence 3129, Application US/10066543
Publication No. US20030087818A1
GENERAL INFORMATION:
APPLICANT: Jiang, Yugu
APPLICANT: Xu, Jiangchun
APPLICANT: Indrias, Carol Joseph
APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
APPLICANT: Carter, Darick
APPLICANT: Fanger, Gary R.
APPLICANT: Smith, Carole L.
APPLICANT: Durham, Margarita
```

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APPLICANT: Stolk, John A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.563
CURRENT APPLICATION NUMBER: US/10/066,543
CURRENT FILING DATE: 2002-01-31
NUMBER OF SEQ ID NOS: 3417
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3129
LENGTH: 446
TYPE: DNA
ORGANISM: Homo sapiens
US-10-066-543-3129

Query Match 6.8%; Score 30; DB 9; Length 446;
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 AAGCACTGATTATGGATATTTTCAGATCAA 233
DB 4 AAGCACTGATTATGGATATTTTCAGATCAA 33

RESULT 6
US-10-046-935-1085
Sequence 1085, Application US/10046935
Patent No. US20020156011A1
GENERAL INFORMATION:
APPLICANT: Jiang, Yugu
APPLICANT: Harlocker, Susan L.
APPLICANT: Secrist, Heather
APPLICANT: Wang, Aijun
APPLICANT: Stolk, John A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.527C1
CURRENT APPLICATION NUMBER: US/10/046,935
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 2239
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1085
LENGTH: 478
TYPE: DNA
ORGANISM: Homo sapiens
US-10-046-935-1085

Query Match 6.8%; Score 30; DB 9; Length 478;
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 AAGCACTGATTATGGATATTTTCAGATCAA 233
DB 189 AAGCACTGATTATGGATATTTTCAGATCAA 218

RESULT 7
US-09-878-178-1085
Sequence 1085, Application US/09878178
Patent No. US20020177552A1
GENERAL INFORMATION:
APPLICANT: Jiang, Yugu
APPLICANT: Harlocker, Susan L.
APPLICANT: Secrist, Heather
APPLICANT: Wang, Aijun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.527
CURRENT APPLICATION NUMBER: US/09/878,178
CURRENT FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 2237
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1085
LENGTH: 478
TYPE: DNA
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ORGANISM: Homo sapiens
US-09-878-178-1085

Query Match 6.8%; Score 30; DB 9; Length 478;
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 AAGCAGTATGATGATATTCAGATCAA 233
DB 189 AAGCAGTATGATGATATTCAGATCAA 218

RESULT 8

US-10-146-502-1085
; Sequence 1085, Application US/10146502
; Publication No. US20030069180A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugui
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Secrist, Heather
; APPLICANT: Wang, Aijun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.527C2
; CURRENT APPLICATION NUMBER: US/10/146,502
; CURRENT FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2241
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1085
; LENGTH: 478
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-146-502-1085

Query Match 6.8%; Score 30; DB 9; Length 478;
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 AAGCAGTATGATGATATTCAGATCAA 233
DB 189 AAGCAGTATGATGATATTCAGATCAA 218

RESULT 9

US-10-102-524-791
; Sequence 791, Application US/10102524
; Publication No. US20030109434A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Gaiger, Alexander
; APPLICANT: Gordon, Brian
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: THERAPY AND METHODS FOR THE
; FILE REFERENCE: 210121.572
; CURRENT APPLICATION NUMBER: US/10/102,524
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 1863
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 791
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 447, 456, 466
; OTHER INFORMATION: n = A,T,C or G
US-10-102-524-791

Query Match 6.8%; Score 30; DB 9; Length 522;
Best Local Similarity 100.0%; Pred. No. 3.6e-06;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 AAGCAGTATGATGATATTCAGATCAA 233
DB 56 AAGCAGTATGATGATATTCAGATCAA 85

RESULT 10

US-10-046-935-1606/C
; Sequence 1606, Application US/10046935
; Patent No. US20020136011A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugui
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Secrist, Heather
; APPLICANT: Wang, Aijun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.527C1
; CURRENT APPLICATION NUMBER: US/10/046,935
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 2239
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1606
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-046-935-1606

Query Match 6.8%; Score 30; DB 9; Length 582;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 AAGCAGTATGATGATATTCAGATCAA 233
DB 511 AAGCAGTATGATGATATTCAGATCAA 482

RESULT 11

US-09-878-178-1606/C
; Sequence 1606, Application US/09878178
; Patent No. US20020177552A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugui
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.527
; CURRENT APPLICATION NUMBER: US/09/878,178
; CURRENT FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 2237
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1606
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-878-178-1606

Query Match 6.8%; Score 30; DB 9; Length 582;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 AAGCAGTATGATGATATTCAGATCAA 233
DB 511 AAGCAGTATGATGATATTCAGATCAA 482

RESULT 12

US-10-146-502-1606/C
; Sequence 1606, Application US/10146502
; Publication No. US20030069180A1

```
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Secrist, Heather
; APPLICANT: Wang, Aljun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.527C2
; CURRENT APPLICATION NUMBER: US/10/146,502
; CURRENT FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2241
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1606
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-146-502-1606

Query Match          6.8%; Score 30; DB 9; Length 582;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 AACGACTGATTATGGATATTTCAGATCAA 233
DB 511 AACGACTGATTATGGATATTTCAGATCAA 482

RESULT 13
US-10-060-036-2544/C
; Sequence 2544, Application US/10060036
; Publication No. US2003007314A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yugu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2544
; LENGTH: 606
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 603
; OTHER INFORMATION: n = A,T,C or G
; US-10-060-036-2544

Query Match          6.8%; Score 30; DB 9; Length 606;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 AACGACTGATTATGGATATTTCAGATCAA 233
DB 511 AACGACTGATTATGGATATTTCAGATCAA 482

RESULT 14
US-09-796-692-8226
; Sequence 8226, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Galger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
```

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; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THE
; TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8226
; LENGTH: 636
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (603)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (615)
; OTHER INFORMATION: n=A,T,C or G
; US-09-796-692-8226

Query Match          6.8%; Score 30; DB 9; Length 636;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 AACGACTGATTATGGATATTTCAGATCAA 233
DB 56 AACGACTGATTATGGATATTTCAGATCAA 85

RESULT 15
US-10-040-862-8226
; Sequence 8226, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Galger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and The
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
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      DATE: 2000-04-27
      APPLICATION NUMBER: US 60/200,303
      PRIOR FILING DATE: 2000-04-28
      PRIOR APPLICATION NUMBER: US 60/200,779
      PRIOR FILING DATE: 2000-04-28
      PRIOR APPLICATION NUMBER: US 60/200,999
      PRIOR FILING DATE: 2000-05-01
      PRIOR APPLICATION NUMBER: US 60/202,084
      PRIOR FILING DATE: 2000-05-04
      PRIOR APPLICATION NUMBER: US 60/206,201
      PRIOR FILING DATE: 2000-05-22
      PRIOR APPLICATION NUMBER: US 60/218,950
      PRIOR FILING DATE: 2000-07-14
      PRIOR APPLICATION NUMBER: US 60/222,903
      PRIOR FILING DATE: 2000-08-03
      PRIOR APPLICATION NUMBER: US 60/223,416
      PRIOR FILING DATE: 2000-08-04
      PRIOR APPLICATION NUMBER: US 60/223,378
      PRIOR FILING DATE: 2000-08-07
      PRIOR APPLICATION NUMBER: US 09/796,692
      PRIOR FILING DATE: 2001-03-01
      NUMBER OF SEQ ID NOS: 10467
      SOFTWARE: FastSeq for Windows Version 3.0
      SEQ ID NO 8226
      LENGTH: 636
      TYPE: DNA
      ORGANISM: Homo sapiens
      FEATURE:
      NAME/KEY: unsure
      LOCATION: (603)
      OTHER INFORMATION: n=A,T,C or G
      FEATURE:
      NAME/KEY: unsure
      LOCATION: (615)
      OTHER INFORMATION: n=A,T,C or G
      US-10-040-862-8226

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Query Match 6.88; Score 30; DB 9; Length 636;
 Best Local Similarity 100.0%; Pred. No. 3.7e-06;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; gaps 0;

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QY 204 AAGCAGTATTGATGATATTTCAGATCAA 233
DB 56 AAGCAGTATTGATGATATTTCAGATCAA 85

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Search completed: July 5, 2003, 07:04:56
 Job time : 132 secs